

**Figure 1A****4.1.1 Heavy Chain DNA**

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ATGGAGTTTG GGCTGAGCTG GGTTCCTC GTTGCTCTTT TAAGAGGTGT 50
CCAGTGTGAG GTGCAGCTGG TGGAGTCTGG GGGAGGCGTG GTCCAGCCTG 100
GGAGGTCCTT GAGACTCTCC TGTGTAGCGT CTGGATTAC CTTAGTAGC 150
CATGGCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC TGGAGTGGGT 200
GGCAGTTATA TGGTATGATG GAAGAAATAA ATACTATGCA GACTCCGTGA 250
AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC GCTGTTTCTG 300
CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTGTATT ACTGTGCGAG 350
AGGAGGTCAC TTCGGTCCTT TTGACTACTG GGGCCAGGGA ACCCTGGTCA 400
CCGTCTCCTC AGCCTCCACC AAGGGCCCAT CGGTCTTCCC CCTGGCGCCC 450
TGCTCCAGGA GCACCTCCGA GAGCACAGCG GCCCTGGGCT GCCTGGTCAA 500
GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA GGCGCTCTGA 550
CCAGCGGCGT GCACACCTTC CCAGCTGTCC TACAGTCCTC AGGACTCTAC 600
TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAACTTCG GCACCCAGAC 650
CTACACCTGC AACGTAGATC ACAAGCCAG CAACACCAAG GTGGACAAGA 700
CAGTTGAGCG CAAATGTTGT GTCGAGTGCC CACCGTGCCC AGCACCACCT 750
GTGGCAGGAC CGTCAGTCTT CCTCTTCCCC CAAAACCCA AGGACACCCT 800
CATGATCTCC CGGACCCCTG AGGTCACGTG CGTGGTGGTG GACGTGAGCC 850
ACGAAGACCC CGAGGTCCAG TTCAACTGGT ACGTGGACGG CGTGGAGGTG 900
CATAATGCCA AGACAAAGCC ACGGGAGGAG CAGTTCAACA GCACGTTCCG 950
TGTGGTCAGC GTCCTCACCG TTGTGCACCA GGACTGGCTG AACGGCAAGG 1000
AGTACAAGTG CAAGGTCTCC AACAAAGGCC TCCCAGCCCC CATCGAGAAA 1050
ACCATCTCCA AAACCAAAGG GCAGCCCCGA GAACCACAGG TGACACCCT 1100
GCCCCATCC CGGGAGGAGA TGACCAAGAA CCAGGTCAGC CTGACCTGCC 1150
TGGTCAAAGG CTTCTACCCC AGCGACATCG CCGTGGAGTG GGAGAGCAAT 1200
GGGCAGCCGG AGAACAACTA CAAGACCACA CCTCCCATGC TGGACTCCGA 1250
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC 1300
AGCAGGGGAA CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC 1350
CACTACACGC AGAAGAGCCT CTCCTGTCT CCGGTAAAT GA 1392

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(SEQ ID NO:27)

**4.1.1 Heavy Chain Protein**

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MEFGLSWVFL VALLRGVQCQ VQLVESGGGV VQPGRSLRLS CVASGFTFSS 50
HGMHWVRQAP GKGLEWVAVI WYDGRNKYYA DSVKGRFTIS RDNSKNTLFL 100
QMNSLRAEDT AVYYCARGGH FGPFYWGQG TLVTVSSAST KGPSVFPLAP 150
CSRSTSESTA ALGCLVKDYF PEPVTVSWNS GALTSGVHTF PAVLQSSGLY 200
SLSSVVTGPS SNFGTQTYTC NVDHKPSNTK VDKTVERKCC VECPPCPAPP 250
VAGPSVFLFP PKPKDTLMIS RTPEVTCVVV DVSHEDPEVQ FNWYVDGVEV 300
HNAKTKPREE QFNSTFRVVS VLTVVHQDWL NGKEYKCKVS NKGLPAPIEK 350
TISKTKGQPR EPQVYTLPPS REEMTKNQVS LTCLVKGFYP SDIAVEWESN 400
GQPENNYKTT PPMLDSGGSF FLYSKLTVDK SRWQQGNVFS CSVMHEALHN 450
HYTQKSLSLG PGK 463

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(SEQ ID NO:1)

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**Figure 1A** (continued)**4.1.1 Kappa Chain DNA**

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ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGGCCAGTCA GAGTATTAGC 150
AGCAGCTTCT TAGCCTGGTA CCAGCAGAGA CCTGGCCAGG CTCCCAGGCT 200
CCTCATCTAT GGTGCATCCA GCAGGGCCAC TGGCATCCCA GACAGGTTCA 250
GTGGCAGTGG GTCTGGGACA GACTTCACTC TCACCATCAG CAGACTGGAG 300
CCTGAAGATT TTGCAGTGTA TTA CTGTCAG CAGTATGGTA CCTCACCCTG 350
GACGTTCCGGC CAAGGGACCA AGGTGGAAAT CAAACGAACT GTGGCTGCAC 400
CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA ATCTGGA ACT 450
GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAG AGGCCAAAGT 500
ACAGTGGAAG GTGGATAACG CCCTCCAATC GGGTAACTCC CAGGAGAGTG 550
TCACAGAGCA GGACAGCAAG GACAGCACCT ACAGCCTCAG CAGCACCCCTG 600
ACGCTGAGCA AAGCAGACTA CGAGAAACAC AAAGTCTACG CCTGCGAAGT 650
CACCCATCAG GGCCTGAGCT CGCCCGTCAC AAAGAGCTTC AACAGGGGAG 700
AGTGTTAG 708

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(SEQ ID NO:40)

**4.1.1 Kappa Chain Protein**

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METPAQLLFL LLLWLPD TTG EIVLTQSPGT LSLSPGERAT LSCRASQ SIS 50
SSFLAWYQQR PGQAPRL LIY GASSRATGIP DRFSGSGSGT DFTLTISRLE 100
PEDFAVYYCQ QYGTSPWTFG QGTKVEIKRT VAAPSVFIFP PSDEQLKSGT 150
ASVVCLLNNF YPREAKVQWK VDNALQSGNS QESVTEQDSK DSTYSLSSTL 200
TLISKADYEKH KVIACEVTHQ GLSSPVT KSF NRGEC 235

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(SEQ ID NO:14)

**Figure 1B****4.8.1 Heavy Chain DNA**

<b>ATGGAGTTTG</b>	<b>GGCTGAGCTG</b>	<b>GGTTTTCTCTC</b>	<b>GTTGCTCTTT</b>	<b>TAAGAGGTGT</b>	50
<b>CCAGTGTCAG</b>	<b>GTGCAGCTGG</b>	<b>TGGAGTCTGG</b>	<b>GGGAGGCGTG</b>	<b>GTCCAGCCTG</b>	100
<b>GGAGGTCCCT</b>	<b>GAGACTCTCC</b>	<b>TGTACAGCGT</b>	<b>CTGGATTAC</b>	<b>CTTCAGTAAC</b>	150
<b>TATGGCATGC</b>	<b>ACTGGGTCCG</b>	<b>CCAGGCTCCA</b>	<b>GGCAAGGGGC</b>	<b>TGGAGTGGGT</b>	200
<b>GGCAGTTATA</b>	<b>TGGTATGATG</b>	<b>GAAGTAATAA</b>	<b>ACACTATGGA</b>	<b>GACTCCGTGA</b>	250
<b>AGGGCCGATT</b>	<b>CACCATCTCC</b>	<b>AGTGACAATT</b>	<b>CCAAGAACAC</b>	<b>GCTGTATCTG</b>	300
<b>CAAATGAACA</b>	<b>GCCTGAGAGC</b>	<b>CGAGGACACG</b>	<b>GCTGTGTATT</b>	<b>ACTGTGCGAG</b>	350
<b>AGGAGAGAGA</b>	<b>CTGGGGTCCT</b>	<b>ACTTTGACTA</b>	<b>CTGGGGCCAG</b>	<b>GGAACCCTGG</b>	400
<b>TCACCGTCTC</b>	<b>CTCAGCCTCC</b>	<b>ACCAAGGGCC</b>	<b>CATCGGTCTT</b>	<b>CCCCCTGGCG</b>	450
<b>CCCTGCTCCA</b>	<b>GGAGCACCTC</b>	<b>CGAGAGCACA</b>	<b>GCGGCCCTGG</b>	<b>GCTGCCTGGT</b>	500
<b>CAAGGACTAC</b>	<b>TTCCCCGAAC</b>	<b>CGGTGACGGT</b>	<b>GTCGTGGAAC</b>	<b>TCAGGCGCTC</b>	550
<b>TGACCAGCGG</b>	<b>CGTGACACCC</b>	<b>TTCCCAGCTG</b>	<b>TCCTACAGTC</b>	<b>CTCAGGACTC</b>	600
<b>TACTCCCTCA</b>	<b>GCAGCGTGGT</b>	<b>GACCGTGCCC</b>	<b>TCCAGCAACT</b>	<b>TCGGCACCCA</b>	650
<b>GACCTACACC</b>	<b>TGCAACGTAG</b>	<b>ATCACAAGCC</b>	<b>CAGCAACACC</b>	<b>AAGGTGGACA</b>	700
<b>AGACAGTTGA</b>	<b>GCGCAAATGT</b>	<b>TGTGTCGAGT</b>	<b>GCCCACCGTG</b>	<b>CCCAGCACCA</b>	750
<b>CCTGTGGCAG</b>	<b>GACCGTCAGT</b>	<b>CTTCCTCTTC</b>	<b>CCCCCAAAC</b>	<b>CCAAGGACAC</b>	800
<b>CCTCATGATC</b>	<b>TCCCGGACCC</b>	<b>CTGAGGTCAC</b>	<b>GTGCGTGGTG</b>	<b>GTGGACGTGA</b>	850
<b>GCCACGAAGA</b>	<b>CCCCGAGGTC</b>	<b>CAGTTCAACT</b>	<b>GGTACGTGGA</b>	<b>CGGCGTGGAG</b>	900
<b>GTGCATAATG</b>	<b>CCAAGACAAA</b>	<b>GCCACGGGAG</b>	<b>GAGCAGTTCA</b>	<b>ACAGCACGTT</b>	950
<b>CCGTGTGGTC</b>	<b>AGCGTCCTCA</b>	<b>CCGTTGTGCA</b>	<b>CCAGGACTGG</b>	<b>CTGAACGGCA</b>	1000
<b>AGGAGTACAA</b>	<b>GTGCAAGGTC</b>	<b>TCCAACAAAG</b>	<b>GCCTCCCAGC</b>	<b>CCCCATCGAG</b>	1050
<b>AAAACCATCT</b>	<b>CCAAAACCAA</b>	<b>AGGGCAGCCC</b>	<b>CGAGAACCAC</b>	<b>AGGTGTACAC</b>	1100
<b>CCTGCCCCCA</b>	<b>TCCCGGGAGG</b>	<b>AGATGACCAA</b>	<b>GAACCAGGTC</b>	<b>AGCCTGACCT</b>	1150
<b>GCCTGGTCAA</b>	<b>AGGCTTCTAC</b>	<b>CCCAGCGACA</b>	<b>TCGCCGTGGA</b>	<b>GTGGGAGAGC</b>	1200
<b>AATGGGCAGC</b>	<b>CGGAGAACAA</b>	<b>CTACAAGACC</b>	<b>ACACCTCCCA</b>	<b>TGCTGGACTC</b>	1250
<b>CGACGGCTCC</b>	<b>TTCTTCCTCT</b>	<b>ACAGCAAGCT</b>	<b>CACCGTGGAC</b>	<b>AAGAGCAGGT</b>	1300
<b>GGCAGCAGGG</b>	<b>GAACGTCTTC</b>	<b>TCATGCTCCG</b>	<b>TGATGCATGA</b>	<b>GGCTCTGCAC</b>	1350
<b>AACCACTACA</b>	<b>CGCAGAAGAG</b>	<b>CCTCTCCCTG</b>	<b>TCTCCGGGTA</b>	<b>AATGA</b>	1395

(SEQ ID NO:28)

**4.8.1 Heavy Chain Protein**

<b>MEFGLSWVFL</b>	<b>VALLRGVQCQ</b>	<b>VQLVESGGGV</b>	<b>VQPGRSLRLS</b>	<b>CTASGFTFSN</b>	50
<b>YGMHWVRQAP</b>	<b>GKGLEWVAVI</b>	<b>WYDGSNKHYG</b>	<b>DSVKGRFTIS</b>	<b>SDNSKNTLYL</b>	100
<b>QMNSLRAEDT</b>	<b>AVYYCARGER</b>	<b>LGSYFDYWGO</b>	<b>GTLVTVSSAS</b>	<b>TKGPSVFPLA</b>	150
<b>PCSRSTSEST</b>	<b>AALGCLVKDY</b>	<b>FPEPVTVSWN</b>	<b>SGALTSGVHT</b>	<b>FPAVLQSSGL</b>	200
<b>YSLSSVVTVP</b>	<b>SSNFGTQTYT</b>	<b>CNVDHKPSNT</b>	<b>KVDKTVERKC</b>	<b>CVECPPCPAP</b>	250
<b>PVAGPSVFLF</b>	<b>PPKPKDTLMI</b>	<b>SRTPEVTCVV</b>	<b>VDVSHEDPEV</b>	<b>QFNWYVDGVE</b>	300
<b>VHNAKTKPRE</b>	<b>EQFNSTFRVV</b>	<b>SVLTVVHQDW</b>	<b>LNGKEYKCKV</b>	<b>SNKGLPAPIE</b>	350
<b>KTISKTKGQP</b>	<b>REPQVYTLPP</b>	<b>SREEMTKNQV</b>	<b>SLTCLVKGFY</b>	<b>PSDIAVEWES</b>	400
<b>NGQPENNYKT</b>	<b>TPPMLDSGDS</b>	<b>FFLYSKLTVD</b>	<b>KSRWQQGNVF</b>	<b>SCSVMHEALH</b>	450
<b>NHYTQKSLSL</b>	<b>SPGK</b>				464

(SEQ ID NO:2)

**Figure 1B** (continued)**4.8.1 Kappa Chain DNA**

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ATGGAAACCC CAGCGCAGCT TCTCTTCCTC CTGCTACTCT GGCTCCCAGA 50
TACCACCGGA GAAATTGTGT TGACGCAGTC TCCAGGCACC CTGTCTTTGT 100
CTCCAGGGGA AAGAGCCACC CTCTCCTGCA GGACCAGTGT TAGCAGCAGT 150
TACTTAGCCT GGTACCAGCA GAAACCTGGC CAGGCTCCCA GGCTCCTCAT 200
CTATGGTGCA TCCAGCAGGG CCACTGGCAT CCCAGACAGG TTCAGTGGCA 250
GTGGGTCTGG GACAGACTTC ACTCTCACCA TCAGCAGACT GGAGCCTGAA 300
GATTTTGCAG TCTATTACTG TCAGCAGTAT GGCATCTCAC CCTTCACTTT 350
CGGCGGAGGG ACCAAGGTGG AGATCAAGCG AACTGTGGCT GCACCATCTG 400
TCTTCATCTT CCCGCCATCT GATGAGCAGT TGAAATCTGG AACTGCCTCT 450
GTTGTGTGCC TGCTGAATAA CTTCTATCCC AGAGAGGCCA AAGTACAGTG 500
GAAGGTGGAT AACGCCCTCC AATCGGGTAA CTCCCAGGAG AGTGTCACAG 550
AGCAGGACAG CAAGGACAGC ACCTACAGCC TCAGCAGCAC CCTGACGCTG 600
AGCAAAGCAG ACTACGAGAA ACACAAAGTC TACGCCTGCG AAGTCACCCA 650
TCAGGGCCTG AGCTCGCCCG TCACAAAGAG CTTCAACAGG GGAGAGTGTT 700
AG 702

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(SEQ ID NO:41)

**4.8.1 Kappa Chain Protein**

```

METPAQLLFL LLLWLPDTTG EIVLTQSPGT LSLSPGERAT LSCRTSVSSS 50
YLAWYQQKPG QAPRLLIYGA SSRATGIPDR FSGSGSGTDF TLTISRLEPE 100
DFAVYYCQQY GISPFTFGGG TKVEIKRTVA APSVFIFPPS DEQLKSGTAS 150
VVCLLN NFYP REAKVQWKVD NALQSGNSQE SVTEQDSKDS TYSLSSTLTL 200
SKADYEKHKV YACEVTHQGL SSPVTKSFNR GEC 233

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(SEQ ID NO:15)

**Figure 1C****4.14.3 Heavy Chain DNA**

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CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTACCAT CTCCAGAGAC AATTCCAAGA AGACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGAACCCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGCG GCGTGCACAC CTTCCAGCT GTCCTACAG 489

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(SEQ ID NO:29)

**4.14.3 Heavy Chain Protein**

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PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAVIWY DGRNKDYADS 50
VKGRFTISR D NSKKTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
LTSGVHTFPA VLQ 163

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(SEQ ID NO:3)

**4.14.3 Kappa Chain DNA**

```

GGCACCCCTGT CTTTGTCTCC AGGGGAAAGA GCCACCCTCT CCTGCAGGGC 50
CAGTCAGAGT GTCAGCAGCT ACTTAGCCTG GTACCAGCAG AAACCTGGCC 100
AGGCTCCCAG ACTCCTCATC TATGGTGCAT CCAGCAGGGC CACTGGCATC 150
CCAGACAGGT TCAGTGGCAG TGGGTCTGGG ACAGACTTCA CTCTCACCAT 200
CAGCAGACTG GAGCCTGAGG ATTTTGCAGT GTATTACTGT CAGCAGTATG 250
GTAGGTCACC ATTCAC TTTC GGCCCTGGGA CCAAAGTGGA TATCAAGCGA 300
ACTGTGGCTG CACCATCTGT CTTTCATCTTC CCGCCATCTG ATGAGCAGTT 350
GAAATCTGGA ACTGCCTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA 400
GAGAGGCCAA AGTACAG 417

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(SEQ ID NO:42)

**4.14.3 Kappa Chain Protein**

```

GTLSPSPGER ATLSCRASQS VSSYLAWYQQ KPGQAPRLLI YGASSRATGI 50
PDRFSGSGSG TDFTLTISR L EPEDFAVYYC QQYGRSPFTF GPGTKVDIKR 100
TVAAPS VFIF PPSDEQLKSG TASVVC LLNN FYPREKVQ 139

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(SEQ ID NO:16)

**Figure 1D****6.1.1 Heavy Chain DNA**

<u>ATGGAGTTTG</u>	<u>GGCTGAGCTG</u>	<u>GGTTTTCTC</u>	<u>GTTGCTCTTT</u>	<u>TAAGAGGTGT</u>	50
CCAGTGTCAG	GTGCAGCTGG	TGGAGTCTGG	GGGAGGCGTG	GTCGAGCCTG	100
GGAGGTCCCT	GAGACTCTCC	TGTACAGCGT	CTGGATTAC	CTTCAGTAGT	150
TATGGCATGC	ACTGGGTCCG	CCAGGCTCCA	GGCAAGGGGC	TGGAGTGGGT	200
GGCAGTTATA	TGGTATGATG	GAAGCAATAA	ACACTATGCA	GACTCCGCGA	250
AGGGCCGATT	CACCATCTCC	AGAGACAATT	CCAAGAACAC	GCTGTATCTG	300
CAAATGAACA	GCCTGAGAGC	CGAGGACACG	GCTGTGTATT	ACTGTGCGAG	350
AGCCGGACTG	CTGGGTTACT	TTGACTACTG	GGGCCAGGGA	ACCCTGGTCA	400
CCGTCTCCTC	AGCCTCCACC	AAGGGCCCAT	CGGTCTTCCC	CCTGGCGCCC	450
TGCTCCAGGA	GCACCTCCGA	GAGCACAGCG	GCCCTGGGCT	GCCTGGTCAA	500
GGACTACTTC	CCCGAACCGG	TGACGGTGTC	GTGGAACCTCA	GGCGCTCTGA	550
CCAGCGGCGT	GCACACCTTC	CCAGCTGTCC	TACAGTCCTC	AGGACTCTAC	600
TCCCTCAGCA	GCGTGGTGAC	CGTGCCCTCC	AGCAACTTCG	GCACCCAGAC	650
CTACACCTGC	AACGTAGATC	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	700
CAGTTGAGCG	CAAATGTTGT	GTCGAGTGCC	CACEGTGCCC	AGCACCACCT	750
GTGGCAGGAC	CGTCAGTCTT	CCTCTTCCCC	CCAAAACCCA	AGGACACCCT	800
CATGATCTCC	CGGACCCCTG	AGGTCACGTG	CGTGGTGGTG	GACGTGAGCC	850
ACGAAGACCC	CGAGGTCCAG	TTCAACTGGT	ACGTGGACGG	CGTGGAGGTG	900
CATAATGCCA	AGACAAAGCC	ACGGGAGGAG	CAGTTCAACA	GCACGTTCCG	950
TGTGGTCAGC	GTCCTCACCG	TTGTGCACCA	GGACTGGCTG	AACGGCAAGG	1000
AGTACAAGTG	CAAGGTCTCC	AACAAAGGCC	TCCCAGCCCC	CATCGAGAAA	1050
ACCATCTCCA	AAACCAAAGG	GCAGCCCCGA	GAACCACAGG	TGTACACCCT	1100
GCCCCCATCC	CGGGAGGAGA	TGACCAAGAA	CCAGGTCAGC	CTGACCTGCC	1150
TGGTCAAAGG	CTTCTACCCC	AGCGACATCG	CCGTGGAGTG	GGAGAGCAAT	1200
GGGCAGCCGG	AGAACAATA	CAAGACCACA	CCTCCCATGC	TGGACTCCGA	1250
CGGCTCCTTC	TTCCTCTACA	GCAAGCTCAC	CGTGGACAAG	AGCAGGTGGC	1300
AGCAGGGGAA	CGTCTTCTCA	TGCTCCGTGA	TGCATGAGGC	TCTGCACAAC	1350
CACTACACGC	AGAAGAGCCT	CTCCCTGTCT	CCGGGTAAAT	GA	1392

(SEQ ID NO:30)

**6.1.1 Heavy Chain Protein**

<u>MEFGLSWVFL</u>	<u>VALLRGVQCQ</u>	<u>VQLVESGGGV</u>	<u>VEPGRSLRLS</u>	<u>CTASGFTFSS</u>	50
YGMHWVRQAP	GKGLEWVAVI	WYDGSNKHYA	DSAKGRFTIS	RDNSKNTLYL	100
QMNSLRAEDT	AVYYCARAGL	LGIFYDYWGQG	TLVTVSSAST	KGPSVFPLAP	150
CSRSTSESTA	ALGCLVKDYF	PEPVTVSWNS	GALTSGVHTF	PAVLQSSGLY	200
SLSSVVTVPS	SNFGTQTYTC	NVDHKPSNTK	VDKTVERKCC	VECPPCPAPP	250
VAGPSVFLFP	PKPKDTLMIS	RTPEVTCVVV	DVSHEDPEVQ	FNWYVDGVEV	300
HNAKTKPREE	QFNSTFRVVS	VLTVVHQDWL	NGKEYKCKVS	NKGLPAPIEK	350
TISKTKGQPR	EPQVYTLPPS	REEMTKNQVS	LTCLVKGFYP	SDIAVEWESN	400
GQPENNYKTT	PPMLDSGGSF	FLYSKLTVDK	SRWQQGNVFS	CSVMHEALHN	450
HYTQKSLSLS	PGK				463

(SEQ ID NO:4)

**Figure 1D** (continued)**6.1.1 Kappa Chain DNA**

<b>ATGGAAACCC</b>	<b>CAGCGCAGCT</b>	<b>TCTCTTCCTC</b>	<b>CTGCTACTCT</b>	<b>GGCTCCCAGA</b>	<b>50</b>
<b>TACCACCGGA</b>	<b>GAAATTGTGT</b>	<b>TGACGCAGTC</b>	<b>TCCAGGCACC</b>	<b>CTGTCTTTGT</b>	<b>100</b>
<b>CTCCAGGGGA</b>	<b>AAGAGCCACC</b>	<b>CTCTCCTGTA</b>	<b>GGGCCAGTCA</b>	<b>AAGTGTTAGC</b>	<b>150</b>
<b>AGCTACTTAG</b>	<b>CCTGGTACCA</b>	<b>ACAGAAACCT</b>	<b>GGCCAGGCTC</b>	<b>CCAGGCCCCT</b>	<b>200</b>
<b>CATCTATGGT</b>	<b>GTATCCAGCA</b>	<b>GGGCCACTGG</b>	<b>CATCCCAGAC</b>	<b>AGGTTCAGTG</b>	<b>250</b>
<b>GCAGTGGGTC</b>	<b>TGGGACAGAC</b>	<b>TTCACTCTCA</b>	<b>CCATCAGCAG</b>	<b>ACTGGAGCCT</b>	<b>300</b>
<b>GAAGATTTTG</b>	<b>CAGTGTATTA</b>	<b>CTGTCAGCAG</b>	<b>TATGGTATCT</b>	<b>CACCATTAC</b>	<b>350</b>
<b>TTTCGGCCCT</b>	<b>GGGACCAAAG</b>	<b>TGGATATCAA</b>	<b>ACGAACTGTG</b>	<b>GCTGCACCAT</b>	<b>400</b>
<b>CTGTCTTCAT</b>	<b>CTTCCCGCCA</b>	<b>TCTGATGAGC</b>	<b>AGTTGAAATC</b>	<b>TGGAAGTGCC</b>	<b>450</b>
<b>TCTGTTGTGT</b>	<b>GCCTGCTGAA</b>	<b>TAAC TTCTAT</b>	<b>CCCAGAGAGG</b>	<b>CCAAAGTACA</b>	<b>500</b>
<b>GTGGAAGGTG</b>	<b>GATAACGCCC</b>	<b>TCCAATCGGG</b>	<b>TAAC TCCCAG</b>	<b>GAGAGTGTCA</b>	<b>550</b>
<b>CAGAGCAGGA</b>	<b>CAGCAAGGAC</b>	<b>AGCACCTACA</b>	<b>GCCTCAGCAG</b>	<b>CACCCTGACG</b>	<b>600</b>
<b>CTGAGCAAAG</b>	<b>CAGACTACGA</b>	<b>GAAACACAAA</b>	<b>GTCTACGCCT</b>	<b>GCGAAGTCAC</b>	<b>650</b>
<b>CCATCAGGGC</b>	<b>CTGAGCTCGC</b>	<b>CCGTCACAAA</b>	<b>GAGCTTCAAC</b>	<b>AGGGGAGAGT</b>	<b>700</b>
<b>GTTAG</b>					<b>705</b>

(SEQ ID NO:43)

**6.1.1 Kappa Chain Protein**

<b>METPAQLLFL</b>	<b>LLLWLPD TTG</b>	<b>EIVLTQSPGT</b>	<b>LSLSPGERAT</b>	<b>LSCRASQSVS</b>	<b>50</b>
<b>SYLAWYQQKP</b>	<b>GQAPRPLIYG</b>	<b>VSSRATGIPD</b>	<b>RFSGSGSGTD</b>	<b>FTLTISRLEP</b>	<b>100</b>
<b>EDFAVYYCQQ</b>	<b>YGISPFTFGP</b>	<b>GTKVDIKRTV</b>	<b>AAPSVFIFPP</b>	<b>SDEQLKSGTA</b>	<b>150</b>
<b>SVVCLLNNFY</b>	<b>PREAKVQWKV</b>	<b>DNALQSGNSQ</b>	<b>ESVTEQDSKD</b>	<b>STYSLSSTLT</b>	<b>200</b>
<b>LSKADYEKHK</b>	<b>VYACEVTHQG</b>	<b>LSSPVTKSFN</b>	<b>RGEC</b>		<b>234</b>

(SEQ ID NO:17)

**Figure 1E****3.1.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TAATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTACAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGGG GCCCGTATAA TAACCCCTTG TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
TCGTGGAAC T CAGGCGCTCT GACCAGCGGC GTGCACACCT TCCCAGCTGT 500
CCTACAG 507

```

(SEQ ID NO:31)

**3.1.1 Heavy Chain Protein**

```

GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APGKGLEWVA VIWYDGSNKY 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARG ARIITPCMDV 100
WGQGTTVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
SWNSGALTSG VHTFPAVLQ 169

```

(SEQ ID NO:5)

**3.1.1 Kappa Chain DNA**

```

CAGTCTCCAT CCTCCCTGTC TGCATCTGTA GGAGACAGAG TCACCATCAC 50
TTGCCGGGCA AGTCAGAGCA TTAACACCTA TTTAATTGG TATCAGCAGA 100
AACCAGGGAA AGCCCCTAAC TTCCTGATCT CTGCTACATC CATTTTGCAA 150
AGTGGGGTCC CATCAAGGTT CCGTGGCAGT GGCTCTGGGA CAAATTTCAC 200
TCTCACCATC AACAGTCTTC ATCCTGAAGA TTTTGCAACT TACTACTGTC 250
AACAGAGTTA CAGTACCCCA TTTACTTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAACGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAGTGGA AGGTGGATAA CGCCCTCCAA 450
TCGGGTAA 458

```

(SEQ ID NO:44)

**3.1.1 Kappa Chain Protein**

```

QSPSSLSASV GDRVITICRA SOSINTYLIW YQQKPGKAPN FLISATSILO 50
SGVPSRFRGS GSGTNFTLTI NSLHPEDFAT YYCQQSYSTP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKVDNALQ 150
SG 152

```

(SEQ ID NO:18)



**Figure 1F****4.10.2 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG TAGCGTCTGG 50
ATTCATCTTC AGTAGTCATG GCATCCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG AAATAAAGAC 150
TATGCAGACT CCGTGAAGGG CCGATTACCC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATTTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCGAGAGTG GCCCCTACTG GGCCACTTGA CTACTGGGGC 300
CAGGGAACCC TGGTCACCGT CTCCTCAGCC TCCACCAAGG GCCCATCGGT 350
CTTCCCCCTG GCGCCCTGCT CCAGGAGCAC CTCCGAGAGC ACAGCGGCCC 400
TGGGCTGCCT GGTCAAGGAC TACTTCCCCG AACCGGTGAC GGTGTCGTGG 450
AACTCAGGCG CTCTGACCAG CGGCGTGCAC ACCTTCCCAG CTGTCCTACA 500
G 501

```

(SEQ ID NO:32)

**4.10.2 Heavy Chain Protein**

```

GVVQPGRSLR LSCVASGFIF SSHGIHWVRQ APGKGLEWVA VIWYDGRNKD 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARV APLGPLDYWG 100
QGTLVTVSSA STKGPSVFPL APCSRSTSES TAALGCLVKD YFPEPVTVSW 150
NSGALTSGVH TFPAVLQ 167

```

(SEQ ID NO:6)

**4.10.2 Kappa Chain DNA**

```

TCTCCAGGCA CCCTGTCTTT GTCTCCAGGG GAAAGAGCCA CCCTCTCCTG 50
CAGGGCCAGT CAGAGTATTA GCAGCAATTT CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATCGTCCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGTTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCATTA TATTACTGTC 250
AGCAGTATGG TACGTCACCA TTCACTTTCG GCCCTGGGAC CAAAGTGGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCCAG AGAGGCCAAA GTACAG 426

```

(SEQ ID NO:45)

**4.10.2 Kappa Chain Protein**

```

SPGTLSSLSPG ERATLSCRAS QSISSNFLAW YQOKPGQAPR LLIYRPSSRA 50
TGIPDSFSGS GSGTDFTLTI SRLEPEDFAL YYCQYGTSP FTFGPGTKVD 100
IKRTVAAPSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQ 142

```

(SEQ ID NO:19)

**Figure 1G****2.1.3 Heavy Chain DNA**

TCGGGCCCAG	GACTGGTGAA	GCCTTCACAG	ATCCTGTCCC	TCACCTGCAC	50
TGTCTCTGGT	GGCTCCATCA	GCAGTGGTGG	TCACTACTGG	AGCTGGATCC	100
GCCAGCACCC	AGGGAAGGGC	CTGGAGTGGA	TTGGGTACAT	CTATTACATT	150
GGGAACACCT	ACTACAACCC	GTCCCTCAAG	AGTCGAGTTA	CCATATCAGT	200
AGACACGTCT	AAGAACCAGT	TCTCCCTGAA	GCTGAGCTCT	GTGACTGCCG	250
CGGACACGGC	CGTGTATTAT	TGTGCGAGAG	ATAGTGGGGA	CTACTACGGT	300
ATAGACGTCT	GGGGCCAAGG	GACCACGGTC	ACCGTCTCCT	CAGCTTCCAC	350
CAAGGGCCCA	TCCGTCTTCC	CCCTGGCGCC	CTGCTCCAGG	AGCACCTCCG	400
AGAGCACAGC	CGCCCTGGGC	TGCCTGGTCA	AGGACTACTT	CCCCGAACCG	450
GTGACGGTGT	CGTGGAAGTC	AGGCGCCCTG	ACCAGCGGCG	TGCACACCTT	500
CCCGGCTGTC	CTACAA				516

(SEQ ID NO:33)

**2.1.3 Heavy Chain Protein**

SGPGLVKPSQ	ILSLTCTVSG	GSISSGGHYW	SWIRQHPGKG	LEWIGYIYYI	50
GNTYYNPSLK	SRVTISVDTS	KNQFSLKLSS	VTAADTAVYY	CARDSGDYYG	100
IDVWGQGTTV	TVSSASTKGP	SVFPLAPCSR	STSESTAALG	CLVKDYFPEP	150
VTVSWNSGAL	TSGVHTFPAV	LQ			172

(SEQ ID NO:7)

**2.1.3 Kappa Chain DNA**

TCTCCAGACT	TTCAGTCTGT	GACTCCAAAG	GAGAAAGTCA	CCATCACCTG	50
CCGGGCCAGT	CAGAGCATTG	GTAGTAGCTT	ACATTGGTAT	CAGCAGAAAC	100
CAGATCAGTC	TCCAAAGCTC	CTCATCAAGT	ATGCTTCCCA	GTCCTTCTCT	150
GGGGTCCCCT	CGAGGTTTCA	TGGCAGTGGA	TCTGGGACAG	ATTTCAACCCT	200
CACCATCAAT	AGCCTGGAAG	CTGAAGATGC	TGCAACGTAT	TACTGTCATC	250
AGAGTAGTAG	TTTACCGCTC	ACTTTCGGCG	GAGGGACCAA	GGTGGAGATC	300
AAACGAACTG	TGGCTGCACC	ATCTGTCTTC	ATCTTCCCGC	CATCTGATGA	350
GCAGTTGAAA	TCTGGAAGTG	CCTCTGTTGT	GTGCCTGCTG	AATAACTTCT	400
ATCCCAGAGA	GGCCAAAGTA	CAGTGGAAGG	TGGATAACGC	CCTCCAATCG	450
GGTAACTCCC	AGGAG				465

(SEQ ID NO:46)

**2.1.3 Kappa Chain Protein**

SPDFQSVTPK	EKVTITCRAS	QSIGSSLHWY	QQKPDQSPKL	LIKYASQSFS	50
GVPSRFSGSG	SGTDFTLTIN	SLEAEDAATY	YCHQSSSLPL	TFGGGKVEI	100
KRTVAAPSVF	IFPPSDEQLK	SGTASVVCLL	NNFYPREAKV	QWKVDNALQS	150
GNSQE					155

(SEQ ID NO:20)

**Figure 1H****4.13.1 Heavy Chain DNA**

```

CCTGGGAGGT CCCTGAGACT CTCCTGTGCA GCGTCTGGAT TCACCTTCAG 50
TAGTCATGGC ATCCACTGGG TCCGCCAGGC TCCAGGCAAG GGGCTGGAGT 100
GGGTGGCAGT TATATGGTAT GATGGAAGAA ATAAAGACTA TGCAGACTCC 150
GTGAAGGGCC GATTCACCAT CTCCAGAGAC AATTCCAAGA ACACGCTGTA 200
TTTGCAAATG AACAGCCTGA GAGCCGAGGA CACGGCTGTG TATTACTGTG 250
CGAGAGTGGC CCCACTGGGG CCACTTGACT ACTGGGGCCA GGAACCCCTG 300
GTCACCGTCT CCTCAGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 350
GCCCTGCTCC AGGAGCACCT CCGAGAGCAC AGCGGCCCTG GGCTGCCTGG 400
TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCT 450
CTGACCAGC 459

```

(SEQ ID NO:34)

**4.13.1 Heavy Chain Protein**

```

PGRSLRLSCA ASGFTFSSHG IHWVRQAPGK GLEWVAWIY DGRNKDYADS 50
VKGRFTISR D NSKNTLYLQM NSLRAEDTAV YYCARVAPLG PLDYWGQGT 100
VTVSSASTKG PSVFPLAPCS RSTSESTAAL GCLVKDYFPE PVTVSWNSGA 150
LTS 153

```

(SEQ ID NO:8)

**4.13.1 Kappa Chain DNA**

```

CAGTCTCCAG GCACCCTGTC TTTGTCTCCA GGGGAAAGAG CCACCCTCTC 50
CTGCAGGGCC AGTCAGAGTG TCAGCAGCTA CTTAGCCTGG TACCAGCAGA 100
AACCTGGCCA GGCTCCCAGG CTCCTCATCT ATGGTGCATC CAGCAGGGCC 150
ACTGGCATCC CAGACAGGTT CAGTGGCAGT GGGTCTGGGA CAGACTTCAC 200
TCTCACCATC AGCAGACTGG AGCCTGAGGA TTTTGCAGTG TATTACTGTC 250
AACAGTATGG TAGGTCACCA TTCACTTTCG GCCCTGGGAC CAAAGTAGAT 300
ATCAAGCGAA CTGTGGCTGC ACCATCTGTC TTCATCTTCC CGCCATCTGA 350
TGAGCAGTTG AAATCTGGAA CTGCCTCTGT TGTGTGCCTG CTGAATAACT 400
TCTATCCAG AGAGGCCAAA GTACAGTGGA AAGGTGATA 440

```

(SEQ ID NO:47)

**4.13.1 Kappa Chain Protein**

```

QSPGTL LSLSP GERATLS CRA SQSVSSYLAW YQKPGQAPR LLIYGASSRA 50
TGIPDR FSGS GSGTDFTLTI SRLEPEDFAV YYCQYGRSP FTFPGPTKVD 100
IKRTVA APSV FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKGG 146

```

(SEQ ID NO:21)

## Figure 11

### 11.2.1 Heavy Chain DNA

GGCGTGGTCC	AGCCTGGGAG	GTCCCTGAGA	CTCTCCTGTG	CAGCGTCTGG	50
ATTCACCTTC	AGTAGCTATG	GCATGCACTG	GGTCCGCCAG	GCTCCAGGCA	100
AGGGGCTGGA	GTGGGTGGCA	GTTATATGGT	ATGATGGAAG	TAATAAATAC	150
TATGCAGACT	CCGTGAAGGG	CCGATTACAC	ATCTCCAGAG	ACAATTCCAA	200
GAACACGCTG	TATCTGCAAA	TGAACAGCCT	GAGAGCCGAG	GACACGGCTG	250
TGTATTACTG	TGCGAGAGAT	CCGAGGGGAG	CTACCCTTTA	CTACTACTAC	300
TACCGGTKGG	ACGTCTGGGG	CCAAGGGACC	ACGGTCACCG	TCTCCTCAGC	350
CTCCACCAAG	GGCCCATCGG	TCTTCCCCCT	GGCGCCCTGC	TCCAGGAGCA	400
CCTCCGAGAG	CACAGCGGCC	CTGGGCTGCC	TGGTCAAGGA	CTACTTCCCC	450
GAACCGGTGA	CGGTGTCGTG	GAACTCAGGC	GCTCTGACCA	GCGGCGTGCA	500
CAC					503

(SEQ ID NO:35)

### 11.2.1 Heavy Chain Protein

GVVQPGRSLR	LSCAASGFTF	SSYGMHWVRQ	APGKGLEWVA	VIWYDGSNKY	50
YADSVKGRFT	ISRDNSKNL	YLQMNSLRAE	DTAVYYCARD	PRGATLYYYY	100
YRXDVWGQGT	TVTVSSASTK	GPSVFPLAPC	SRSTSESTAA	LGCLVKDYFP	150
EPVTVSWNSG	ALTSGVH				167

(SEQ ID NO:9)

### 11.2.1 Kappa Chain DNA

CCATCCTCCC	TGTCTGCATC	TGTAGGAGAC	AGAGTCACCA	TCACTTGCCG	50
GGCAAGTCAG	AGCATTAACA	GCTATTTAGA	TTGGTATCAG	CAGAAACCAG	100
GGAAAGCCCC	TAAACTCCTG	ATCTATGCTG	CATCCAGTTT	GCAAAGTGGG	150
GTCCCATCAA	GGTTCAGTGG	CAGTGGATCT	GGGACAGATT	TCACTCTCAC	200
CATCAGCAGT	CTGCAACCTG	AAGATTTTGC	AACTTACTAC	TGTCAACAGT	250
ATTACAGTAC	TCCATTCACT	TTCGGCCCTG	GGACCAAAGT	GGAAATCAAA	300
CGAACTGTGG	CTGCACCATC	TGTCTTCATC	TTCCCGCCAT	CTGATGAGCA	350
GTTGAAATCT	GGAAGTGCCT	CTGTTGTGTG	CCTGCTGAAT	AACTTCTATC	400
CCAGAGAGGC	CAAAGTA				417

(SEQ ID NO:48)

### 11.2.1 Kappa Chain Protein

PSSLSASVGD	RVTITCRASQ	SINSYLDWYQ	QKPGKAPKLL	IYAASSLQSG	50
VPSRFSGSGS	GTDFTLTISS	LOPEDFATYY	CQOYYSTPFT	FGPGTKVEIK	100
RTVAAPSVFI	FPPSDEQLKS	GTASVVCLLN	NFYPPREAKV		139

(SEQ ID NO:22)

**Figure 1J****11.6.1 Heavy Chain DNA**

```

GGCGTGGTCC AGCCTGGGAG GTCCCTGAGA CTCTCCTGTG CAGCGTCTGG 50
ATTCACCTTC AGTAGCTATG GCATGCACTG GGTCCGCCAG GCTCCAGGCA 100
AGGGGCTGGA GTGGGTGGCA GTTATATGGT ATGATGGAAG TCATAAATAC 150
TATGCAGACT CCGTGAAGGG CCGATTACAC ATCTCCAGAG ACAATTCCAA 200
GAACACGCTG TATCTGCAAA TGAACAGCCT GAGAGCCGAG GACACGGCTG 250
TGTATTACTG TGCAGAGAGG GCTGTAGTAG TACCAGCTGC TATGGACGTC 300
TGGGGCCAAG GGACCACGGT CACCGTCTCC TCAGCCTCCA CCAAGGGCCC 350
ATCGGTCTTC CCCCTGGCGC CCTGCTCCAG GAGCACCTCC GAGAGCACAG 400
CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 450
T 451

```

(SEQ ID NO:36)

**11.6.1 Heavy Chain Protein**

```

GVVQPGRSLR LSCAASGFTF SSYGMHWVRQ APKGKLEWVA VIWYDGSHKY 50
YADSVKGRFT ISRDNSKNTL YLQMNSLRAE DTAVYYCARG AVVVPAAMDV 100
WGQGTTVTVS SASTKGPSVF PLAPCSRSTS ESTAALGCLV KDYFPEPVTV 150
S 151

```

(SEQ ID NO:10)

**11.6.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA ACATTAGCAG GTATTTAAAT TGGTATCAAC 100
AGAAACCAGG GAAAGCCCCT AAGTTCCTGA TCTATGTTGC ATCTATTTTG 150
CAAAGTGGGG TCCCATCAGG GTTCAGTGCC AGTGGATCTG GGCCAGATTT 200
CACTCTNACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACAGTACC CCATTCACTT TCGGCCCTGG GACCAAAGTG 300
GATATCAAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA 400
AC 402

```

(SEQ ID NO:49)

**11.6.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITICR ASQNISRYLN WYQQKPGKAP KFLIYVASIL 50
QSGVPSGFSV SGSGPDFTLT ISSLOPEDFA TYQCQSYST PFTFGPGTKV 100
DIKRTVAAPS VFIFPPSDEQ LKSGTASVVC LLNN 134

```

(SEQ ID NO:23)

**Figure 1K****11.7.1 Heavy Chain DNA**

```

GTGGTCCAGC CTGGGAGGTC CCTGAGACTC TCCTGTGCAG CGTCTGGATT 50
CACCTTCAGT AGCNGTGGCA TGCAGTGGGT CCGCCAGGCT CCAGGCAAGG 100
GGCTGGAGTG GGTGGCAGTT ATATGGTCTG ATGGAAGTCA TAAATACTAT 150
GCAGACTCCG TGAAGGGCCG ATTCACCATC TCCAGAGACA ATTCCAAGAA 200
CACGCTGTAT CTGCAAATGA ACAGCCTGAG AGCCGAGGAC ACGGCTGTGT 250
ATTACTGTGC GAGAGGAACT ATGATAGTAG TGGGTACCCT TGACTACTGG 300
GGCCAGGGAA CCCTGGTCAC CGTCTCCTCA GCCTCCACCA AGGGCCCATC 350
GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCCGAG AGCACAGCGG 400
CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCG 438

```

(SEQ ID NO:37)

**11.7.1 Heavy Chain Protein**

```

VVQPGRSLRL SCAASGFTFS SXGMHWVRQA PGKGLEWVAV IWSDGSHKYY 50
ADSVKGRFTI SRDNSKNTLY LQMNSLRAED TAVYYCARGT MIVVGTLDYW 100
GQGTLLTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEP 146

```

(SEQ ID NO:11)

**11.7.1 Kappa Chain DNA**

```

ACCCAGTCTC CATCCTCCCT GTCTGCATCT GTAGGAGACA GAGTCACCAT 50
CACTTGCCGG GCAAGTCAGA GCATTTGCAA CTATTTAAAT TGGTATCAGC 100
AGAAACCAGG AAAAGCCCTT AGGGTCCTGA TCTATGCTGC ATCCAGTTTG 150
CAAGGTGGGG TCCCGTCAAG GTTCAGTGGC AGTGGATCTG GGACAGATTG 200
CACTCTCACC ATCAGCAGTC TGCAACCTGA AGATTTTGCA ACTTACTACT 250
GTCAACAGAG TTACACTACC CCATTCACCT TCGGCCCTGG GACCAGAGTG 300
GATATCGAAC GAACTGTGGC TGCACCATCT GTCTTCATCT TCCCGCCATC 350
TGATGAGCAG TTGAAATCTG GAACTGCCTC TGTTGTGTGC CTGCTGAATA 400
ACTTCTATCC CAGAGAGGCC AAAGTACAGT GGAAGGTGGA TAACGCCTAT 450
T 451

```

(SEQ ID NO:50)

**11.7.1 Kappa Chain Protein**

```

TQSPSSLSAS VGDRVITICR ASQSICNYLN WYQQKPGKAP RVLIYAASSL 50
QGGVPSRFSG SGSGIDCTLT ISSLQPEDFA TYQCQSYIT PFTFGPGTRV 100
DIERTVAAPS VFIFPPSDEQ LKSGTASVVC LLNNFYPREA KVQWKVDNAY 150

```

(SEQ ID NO:24)

**Figure 1L****12.3.1.1 Heavy Chain DNA**

TCCTGTGCAG	CGTCTGGATT	CACCTTCAGT	TACTATGGCG	TCTGGGGGAG	50
GCGTGGTCCA	GCCTGGGAGG	TCCCTGAGAC	TCTCCTGTGC	AGCGTCTGGA	100
TTCACCTTCA	GTAGCTATGG	CGTGCACTGG	GTCCGCCAGG	CTCCAGGCAA	150
GGGGCTGGAG	TGGGTGGCAG	TTATATGGTA	TGATGGAAGT	AATAAATACT	200
ATGCAGACTC	CGTGAAGGGC	CGATTCACCA	TCTCCAGAGA	CAATTCCAAG	250
AGCACGCTGT	ATCTGCAAAT	GAACAGCCTG	AGAGCCGAGG	ACACGGCTGT	300
GTATTATTGT	GCGAGAGACT	CGTATTACGA	TTTTTGGAGT	GGTCGGGGCG	350
GTATGGACGT	CTGGGGGCCAA	GGGACCACGG	TCACCGTCTC	CTCAGCCTCC	400
ACCAAGGGCC	CATCGGTCTT	CCCCCTGGCG	CCCTGCTCCA	GGAGCACCTC	450
CGAGAGCACA	GCGGCCCTGG	GCTGCCTGGT	CAAGGACTAC	TTCCCCGAAC	500
CGGTGACGGT	GTCGTGGAAC	TCAGGCGCTC	TGACCAGCGG	CGTGCACACC	550
TTCCCAGCTG	TC				562

(SEQ ID NO:38)

**12.3.1.1 Heavy Chain Protein**

SGGGVVQPGR	SLRLSCAASG	FTFSSYGVHW	VRQAPGKGLE	WVAVIWYDGS	50
NKYADSVKG	RFTISRDNK	STLYLQMNLS	RAEDTAVYYC	ARDSYYDFWS	100
GRGGMDVWQ	GTTVTVSSAS	TKGPSVFPLA	PCSRSTSEST	AALGCLVKDY	150
FPEPVTVSWN	SGALTSGVHT	FPAV			174

(SEQ ID NO:12)

**12.3.1.1 Kappa Chain DNA**

CCACTCTCCC	TGCCCCGTCAC	CCTTGGACAG	CCGGCCTCCA	TCTCCTGCAG	50
GTCTAGTCAA	AGCCTCGTAT	ACAGTGATGG	AAACACCTAC	TTGAATTGGT	100
TTCAGCAGAG	GCCAGGCCAA	TCTCCAAGGC	GCCTAATTTA	TAAGGTTTCT	150
AACTGGGACT	CTGGGGTCCC	AGACAGATTC	AGCGGCAGTG	GGTCAGGCAC	200
TGATTTTACA	CTGAAAATCA	GCAGGGTGGG	GGCTGAGGAT	GTTGGGGTTT	250
ATTACTGCAT	GCAAGGTTCA	CACTGGCCTC	CGACGTTTCG	CCAAGGGACC	300
AAGGTGGAAA	TCAAACGAAC	TGTGGCTGCA	CCATCTGTCT	TCATCTTCCC	350
GCCATCTGAT	GAGCAGTTGA	AATCTGGAAC	TGCCTCTGTT	GTGTGCCTGC	400
TGAATAACTT	CTATCCCAC				419

(SEQ ID NO:51)

**12.3.1.1 Kappa Chain Protein**

PLSLPVTLGQ	PASISCRSSQ	SLVYSDGNTY	LNWFQQRPGQ	SPRRLIYKVS	50
NWDSGVPDRF	SGSGSGTDFT	LKISRVEAED	VGVIYCMQGS	HWPPTFGQGT	100
KVEIKRTVAA	PSVFIFPPSD	EQLKSGTASV	VCLLNNFYF		139

(SEQ ID NO:25)

**Figure 1M****12.9.1.1 Heavy Chain DNA**

```

GTCCAGCCTG GGAGGTCCCT GAGACTCTCC TGTGCAGCGT CTGGATTACAC 50
CTTCAGTAAC TATGCCATGC ACTGGGTCCG CCAGGCTCCA GGCAAGGGGC 100
TGGAGTGGGT GGTAGTTATT TGGCATGATG GAAATAATAA ATACTATGCA 150
GAGTCCGTGA AGGGCCGATT CACCATCTCC AGAGACAATT CCAAGAACAC 200
GCTGTATCTG CAAATGAACA GCCTGAGAGC CGAGGACACG GCTGTATATT 250
ACTGTGCGAG AGATCAGGGC ACTGGCTGGT ACGGAGGCTT TGACTTCTGG 300
GGCCAGGGAA CCCTGGTCAC CGTCTCCTCA GCCTCCACCA AGGGCCCATC 350
GGTCTTCCCC CTGGCGCCCT GCTCCAGGAG CACCTCCGAG AGCACAGCGG 400
CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG 450
TGGAACTCAG GCGCTCTGAC CAGCGGCGTG CACACCTTCC 490

```

(SEQ ID NO:39)

**12.9.1.1 Heavy Chain Protein**

```

VQGRSLRLS CAASGFTFSN YAMHWVRQAP GKGLEWVVVI WHDGNNKYIA 50
ESVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCARDQG TGWYGGFDFW 100
GQGLTVTVSS ASTKGPSVFP LAPCSRSTSE STAALGCLVK DYFPEPVTVS 150
WNSGALTSGV HTF 163

```

(SEQ ID NO:13)

**12.9.1.1 Kappa Chain DNA**

```

CCTGGAGAGC CGGCTTCCAT CTCTTGACAG TCTAGTCAGA GCCTCCTGCA 50
TAGTAATGGA TACAACATATT TGGATTGGTA CCTGCAGAAG CCAGGACAGT 100
CTCCACAGCT CCTGATCTAT TTGGGTTCTA ATCGGGCCTC CGGGGTCCCT 150
GACAGGTTCA GTGGCAGTGG ATCAGGCACA GATTTTACAC TGAAACTCAG 200
CAGAGTGGAG GCTGAGGATG TTGGGGTTTA TTACTGCATG CAAGCTCTAC 250
AAACTCCTCT CACTTTCGGC GGAGGGACCA AGGTGGAGAT CAAACGAACT 300
GTGGCTGCAC CATCTGTCTT CATCTTCCCG CCATCTGATG AGCAGTTGAA 350
ATCTGGAAGT GCCTCTGTTG TGTGCCTGCT GAATAACTTC TATCCCAGAR 400
AGGCCAAAGT ACATTCCAT 419

```

(SEQ ID NO:52)

**12.9.1.1 Kappa Chain Protein**

```

PGEPAISCR SSQSLHLSNG YNYLDWYLQK PGQSPQLLIY LGSNRASGVP 50
DRFSGSGSGT DFTLKLRSVE AEDVGVIYCM QALQTPLTFG GGTKVEIKRT 100
VAAPSVFIFP PSDEQLKSGT ASVVCLLNNF YPR 133

```

(SEQ ID NO:26)



**Figure 2A**

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
								G					
	G	G	G	G	G			G	G	G		G	
	V	V	V	V	V			V	V	V	V	V	
	V	V	V	V	V			V	V	V	V	V	V
	Q	Q	Q	Q	Q			E	Q	Q	Q	Q	Q
	P	P	P	P	P	P	P	P	P	P	P	P	P
	G	G	G	G	G	G	G	G	G	G	G	G	G
	R	R	R	R	R	R	R	R	R	R	R	R	R
	S	S	S	S	S	S	S	S	S	S	S	S	S
	L	L	L	L	L	L	L	L	L	L	L	L	L
	R	R	R	R	R	R	R	R	R	R	R	R	R
	L	L	L	L	L	L	L	L	L	L	L	L	L
	S	S	S	S	S	S	S	S	S	S	S	S	S
	C	C	C	C	C	C	C	C	C	C	C	C	C
	A	A	V	T	V	A	A	T	A	A	A	A	A
	A	A	A	A	A	A	A	A	A	A	A	A	A
	S	S	S	S	S	S	S	S	S	S	S	S	S
	G	G	G	G	G	G	G	G	G	G	G	G	G
	F	F	F	F	F	F	F	F	F	F	F	F	F
	T	T	T	T	I	T	T	T	T	T	T	T	T
	F	F	F	F	F	F	F	F	F	F	F	F	F
CDR1	S	S	S	S	S	S	S	S	S	S	S	S	S
	S	S	S	N	S	S	S	S	S	S	S	S	N
	Y	Y	H	Y	H	H	H	Y	Y	Y	C	Y	Y
	G	G	G	G	G	G	G	G	G	G	G	G	A
	M	M	M	M	I	I	I	M	M	M	M	V	M
	H	H	H	H	H	H	H	H	H	H	H	H	H
	W	W	W	W	W	W	W	W	W	W	W	W	W
	V	V	V	V	V	V	V	V	V	V	V	V	V
	R	R	R	R	R	R	R	R	R	R	R	R	R
	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
	A	A	A	A	A	A	A	A	A	A	A	A	A
	P	P	P	P	P	P	P	P	P	P	P	P	P
	G	G	G	G	G	G	G	G	G	G	G	G	G
	K	K	K	K	K	K	K	K	K	K	K	K	K
	G	G	G	G	G	G	G	G	G	G	G	G	G
	L	L	L	L	L	L	L	L	L	L	L	L	L
	E	E	E	E	E	E	E	E	E	E	E	E	E
	W	W	W	W	W	W	W	W	W	W	W	W	W
	V	V	V	V	V	V	V	V	V	V	V	V	V
	A	A	A	A	A	A	A	A	A	A	A	A	V
	V	V	V	V	V	V	V	V	V	V	V	V	V
	I	I	I	I	I	I	I	I	I	I	I	I	I
	W	W	W	W	W	W	W	W	W	W	W	W	W
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	S	Y	H
	D	D	D	D	D	D	D	D	D	D	D	D	D
	G	G	G	G	G	G	G	G	G	G	G	G	G
CDR2	S	S	R	S	R	R	R	S	S	S	S	S	N

**Figure 2B**

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
	N	N	N	N	N	N	N	N	N	H	H	N	N
	K	K	K	K	K	K	K	K	K	K	K	K	K
	Y	Y	Y	H	D	D	D	H	Y	Y	Y	Y	Y
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	A	A	A	G	A	A	A	A	A	A	A	A	A
	D	D	D	D	D	D	D	D	D	D	D	D	E
	S	S	S	S	S	S	S	S	S	S	S	S	S
	V	V	V	V	V	V	V	A	V	V	V	V	V
	K	K	K	K	K	K	K	K	K	K	K	K	K
	G	G	G	G	G	G	G	G	G	G	G	G	G
	R	R	R	R	R	R	R	R	R	R	R	R	R
	F	F	F	F	F	F	F	F	F	F	F	F	F
	T	T	T	T	T	T	T	T	T	T	T	T	T
	I	I	I	I	I	I	I	I	I	I	I	I	I
	S	S	S	S	S	S	S	S	S	S	S	S	S
	R	R	R	S	R	R	R	R	R	R	R	R	R
	D	D	D	D	D	D	D	D	D	D	D	D	D
	N	N	N	N	N	N	N	N	N	N	N	N	N
	S	S	S	S	S	S	S	S	S	S	S	S	S
	K	K	K	K	K	K	K	K	K	K	K	K	K
	N	N	N	N	N	N	K	N	N	N	N	S	N
	T	T	T	T	T	T	T	T	T	T	T	T	T
	L	L	L	L	L	L	L	L	L	L	L	L	L
	Y	Y	F	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	L	L	L	L	L	L	L	L	L	L	L	L	L
	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q	Q
	M	M	M	M	M	M	M	M	M	M	M	M	M
	N	N	N	N	N	N	N	N	N	N	N	N	N
	S	S	S	S	S	S	S	S	S	S	S	S	S
	L	L	L	L	L	L	L	L	L	L	L	L	L
	R	R	R	R	R	R	R	R	R	R	R	R	R
	A	A	A	A	A	A	A	A	A	A	A	A	A
	E	E	E	E	E	E	E	E	E	E	E	E	E
	D	D	D	D	D	D	D	D	D	D	D	D	D
	T	T	T	T	T	T	T	T	T	T	T	T	T
	A	A	A	A	A	A	A	A	A	A	A	A	A
	V	V	V	V	V	V	V	V	V	V	V	V	V
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y
	C	C	C	C	C	C	C	C	C	C	C	C	C
	A	A	A	A	A	A	A	A	A	A	A	A	A
	R	R	R	R	R	R	R	R	R	R	R	R	R
		G	G	G	V	V	V	A	D	G	G	D	D
		A	G	E	A	A	A	G	P	A	T	S	Q
		R	H	R	P	P	P	L	R	V	M	Y	G
		I	F	L	L	L	L	L	G	V	I	Y	T
CDR3		I	G	G	G	G	G	G	A	V	V	D	G

**Figure 2C**

CDR	DP5 0	3.1.1	4.1.1	4.8.1	4.10. 2	4.13. 1	4.14. 3	6.1.1	11.2. 1	11.6. 1	11.7. 1	12.3. 1.1	12.9. 1.1
		T	P	S	P	P	P	Y	T	P	V	F	W
		P	F	Y	L	L	L	F	L	A	G	W	Y
		C	D	F	D	D	D	D	Y	A	T	S	G
		M	Y	D	Y	Y	Y	Y	Y	M	L	G	G
		D	W	Y	W	W	W	W	Y	D	D	R	F
		V	G	W	G	G	G	G	Y	V	Y	G	D
		W	Q	G	Q	Q	Q	Q	Y	W	W	G	F
		G	G	Q	G	G	G	G	G	G	G	M	W
		Q	T	G	T	T	T	T	M	Q	Q	D	G
		G	L	T	L	L	L	L	D	G	G	V	Q
		T	V	L	V	V	V	V	V	T	T	W	G
		T	T	V	T	T	T	T	W	T	L	G	T
		V	V	T	V	V	V	V	G	V	V	Q	L
		T	S	V	S	S	S	S	Q	T	T	G	V
		V	S	S	S	S	S	S	G	V	V	T	T
		S	A	S	A	A	A	A	T	S	S	T	V
		S	S	A	S	S	S	S	T	S	S	V	S
		A	T	S	T	T	T	T	V	A	A	T	S
		S	K	T	K	K	K	K	T	S	S	V	A
		T	G	K	G	G	G	G	V	T	T	S	S
		K	P	G	P	P	P	P	S	K	K	S	T
		G	S	P	S	S	S	S	S	G	G	A	K
		P	V	S	V	V	V	V	A	P	P	S	G
		S	F	V	F	F	F	F	S	S	S	T	P
		V	P	F	P	P	P	P	T	V	V	K	S
		F	L	P	L	L	L	L	K	F	F	G	V
		P	A	L	A	A	A	A	G	P	P	P	F
		L	P	A	P	P	P	P	P	L	L	S	P
		A	C	P	C	C	C	C	S	A	A	V	L
		P	S	C	S	S	S	S	V	P	P	F	A
		C	R	S	R	R	R	R	F	C	C	P	P
		S	S	R	S	S	S	S	P	S	S	L	C
		R	T	S	T	T	T	T	L	R	R	A	S
		S	S	T	S	S	S	S	A	S	S	P	R
		T	E	S	E	E	E	E	P	T	T	C	S
		S	S	E	S	S	S	S	C	S	S	S	T
		E	T	S	T	T	T	T	S	E	E	R	S
		S	A	T	A	A	A	A	R	S	S	S	E
		T	A	A	A	A	A	A	S	T	T	T	S
		A	L	A	L	L	L	L	T	A	A	S	T
		A	G	L	G	G	G	G	S	A	A	E	A
		L	C	G	C	C	C	C	E	L	L	S	A
		G	L	C	L	L	L	L	S	G	G	T	L
		C	V	L	V	V	V		T	C	C	A	G
		L	K	V	K	K	K		A	L	L	A	C
		V	D	K	D	D	D		A	V	V	L	L
		K	Y	D	Y	Y	Y		L	K	K	G	V
		D	F	Y	F	F	F		G	D	D	C	K
		Y	P	F	P	P	P		C	Y	Y	L	D

**Figure 2D**

[illegible]

## Figure 3

### DP-65 or 4-31 gene product

VSGGSISSGGYYW<sup>CDR1</sup>SWIRQHPGKGLEWIGYIYVSGSTIYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR<sup>CDR2</sup>

### 2.1.3 Heavy Chain Protein

SGPGLVKPSQILSLTCTVSGGSISGGHYVSWIRQHPGKGLEWIGYIYIYGNYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAR<sup>CDR1</sup>  
DSGDYYGIDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ<sup>CDR2</sup>  
<sup>CDR3</sup>

## Figure 4

### A27 Gene Product

EIVLTQSPGTLSLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGSSP  
 CDR1 CDR2 CDR3

### 4.1.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSISSSELA WYQQRPQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGTSPWT  
 CDR1 CDR2 CDR3  
 FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK

### 4.8.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRISQVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.14.3 Kappa Chain Protein

GTLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FPGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 6.1.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGVSRRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGISPET  
 CDR1 CDR2 CDR3  
 FPGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.10.2 Kappa Chain Protein

SPGTLSLSPGERATLSCRASQSISSNELA WYQQKPGQAPRLIYRPSRATGIPDRFSGSGGTDFTLTISRLEPEDFALYYCQOYGTSPET  
 CDR1 CDR2 CDR3  
 FPGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQ

### 4.13.1 Kappa Chain Protein

QSPGTLSLSPGERATLSCRASQSVSSSYLA WYQQKPGQAPRLIYGASSRATGIPDRFSGSGGTDFTLTISRLEPEDFAVYYCQOYGRSPET  
 CDR1 CDR2 CDR3  
 FPGGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKGG

## Figure 5

### 012 Gene Product

DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNIWYQQKPKGAPKLLIYAASSLQSGVPSRFRSGSGTDFTLTISSLQPEDFATYYCQQQSYSTP  
 CDR1 CDR2 CDR3

### 3.1.1 Kappa Chain Protein

QSPSSLSASVGDRVTITCRASQSIINTYLIWYQQKPKGAPNFI~~LSAT~~SILOSGVPSRFRSGSGTNFTLTINSLHPEDFATYYCQQQSYSTPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG

### 11.2.1 Kappa Chain Protein

PSSLSASVGDRVTITCRASQSIINSYLLDWYQQKPKGAPKLLIYAASSLQSGVPSRFRSGSGTDFTLTISSLQPEDFATYYCQQQY~~YSTPET~~  
 CDR1 CDR2 CDR3  
 FGPGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKV

### 11.6.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASONISRYLNIWYQQKPKGAPKFLIYV~~AS~~SILOSGVPSGFSA~~SG~~SGPDFTLTISSLQPEDFATYYCQQQSYSTPET  
 CDR1 CDR2 CDR3  
 FGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNN

### 11.7.1 Kappa Chain Protein

TQSPSSLSASVGDRVTITCRASQSI~~CN~~YLNWYQQKPKGAPRVLIYAASSLQGGVPSRFRSGSGIDCTLTISSLQPEDFATYYCQQQSY~~ITPET~~  
 CDR1 CDR2 CDR3  
 FGPGTRVDIERTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAY

## Figure 6

### A10/A26 Gene Product

EVL TQSPDFQSVTPKEKVTITCRASQSIGSSLLHWYQQKPDQSPKLLIKYASQSESGVPSRFGSGSGTDFTLTINSLEAEDAATYYCHQSSSLPQ  
CDR1 CDR2 CDR3

### 2.1.3 Kappa Chain Protein

SPDFQSVTPKEKVTITCRASQSIGSSLLHWYQQKPDQSPKLLIKYASQSESGVPSRFGSGSGTDFTLTINSLEAEDAATYYCHQSSSLPLT  
CDR1 CDR2 CDR3  
FGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQE



## Figure 7

### A17 Gene Product

DVVMTQSP~~LSLPVT~~LGQPA~~SISCRSSQSLVYS~~DGNT~~YLNWFQ~~RPQSP~~RRLYKVS~~NRD~~SGVPDR~~FSGSGGT~~DFTLKISR~~VEAEDVGVYY~~CMQ~~GTHWP  
CDR1 CDR2 CDR3

### 12.3.1 Kappa Chain Protein

PLSLPVT~~LGQPA~~SISCRSSQSLVYS~~DGNTYLNWFQ~~RPQSP~~RRLYKVS~~NRD~~SGVPDR~~FSGSGGT~~DFTLKISR~~VEAEDVGVYY~~CMQ~~GSHWPPT  
CDR1 CDR2 CDR3  
FGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYP

## Figure 8

### A3/A19 Gene Product

DI~~V~~MTQSP~~L~~SLPVT~~P~~GE~~P~~ASISCRSSQSL~~L~~HSNGYN~~Y~~LDWY~~L~~QKPGQSPQ~~L~~LI~~Y~~LGSN~~R~~ASGV~~P~~DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQA~~L~~QT~~P~~  
CDR1 CDR2 CDR3

### 12.2.1 Kappa Chain Protein

PGEPASISCRSSQSL~~L~~HSNGYN~~Y~~LDWY~~L~~QKPGQSPQ~~L~~LI~~Y~~LGSN~~R~~ASGV~~P~~DRFSGSGSGTDFTLKISRVEAEDVGVYYCMQA~~L~~QT~~P~~LT  
CDR1 CDR2 CDR3

**Figure 9** Amino-terminal amino acid sequence analysis

Hybridoma	Light chain	MW
CT2.1.3	ND	ND
CT3.1.1	NH <sub>2</sub> -DIQMTQSPSSLSASVGDRV	26,119
CT4.1.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,917
CT4.8.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,617
CT4.9.1	NH <sub>2</sub> -DIQMTQSPSSVSASVGDRV	23,702
CT4.10.2	NH <sub>2</sub> -TGEFVLTQSPGTLSPGER (60%) NH <sub>2</sub> -EFVLTQSPGTLSPGERAT (40%)	24,101
CT4.14.3	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,770
CT4.13.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,802
CT6.1.1	NH <sub>2</sub> -EIVLTQSPGTLSPGERAT	23,747

Hybridoma	Heavy chain	MW
CT2.1.3	ND	ND
CT3.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~80%) NH <sub>2</sub> -PEVQF...(minor sequence~20%)	51,813
CT4.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~65%) NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~35%)	51,502
CT4.8.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPG(R)SL... (major sequence~60%) NH <sub>2</sub> -PEVQFNWY...(minor sequence~40%)	51,597
CT4.9.1	NH <sub>2</sub> -EVQLLESGGGLVQPGGSLRL (free amino terminus)	51,437
CT4.10.2	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~60%) NH <sub>2</sub> -PEVQFNWYVD...(minor sequence~40%)	51,502
CT4.14.3	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSL(R)(L)(S) (major sequence~65%) NH <sub>2</sub> -PEVQFNWYV...(minor sequence~35%)	51,293
CT4.13.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVQPGRSLRLS (major sequence~75%) NH <sub>2</sub> -PEVQFN...(minor sequence~25%)	51,305
CT6.1.1	NH <sub>2</sub> -Blocked. Following treatment with Pyroglutamate Aminopeptidase: NH <sub>2</sub> -pQ-VQLVESGGGVVEPGRSLRLS* (major sequence~65%) NH <sub>2</sub> -PEVQFNWYVD... (minor sequence~35%)	51,476

\* This heavy chain sequence is similar to the other blocked heavy chain sequences except for a unique Gln->Glu change at position 13.

Figure 10A

antibody	Conc. (mg/ml) (Ec1.58)		IEF	SDS-PAGE		SEC	reported MALDI		n-term. seq. (lc)*	
	reported	observed		(+) b-me	(-) b-me		Hc	Lc	reported	observed
CT 3.1.1	1.1	1.57	smear	50 & 28 kDa	6 bands	139,400	51,813	26,119	DIQMTQSP (SEQ ID NO: 141)	DIQMTQSP (SEQ ID NO: 141)
CT 4.1.1	1.54	1.65	smear	50 & 24 kDa	6 bands	79,900	51,502	23,917	EIVLTQSP (SEQ ID NO: 142)	EIVLTQSP (SEQ ID NO: 142)
CT 4.8.1	1.52	1.54	4 bands	50 & 24 kDa	6 bands	110,300	51,597	23,617	EIVLTQSP (SEQ ID NO: 143)	EIVLTQSP (SEQ ID NO: 143)
CT 4.10.2	1.29	1.77	4 bands	50 & 25 kDa	6 bands	107,200	51,502	24,101	**	***
CT 4.14.3	1.75	1.65	smear	50 & 24 kDa	6 bands	82,800	51,293	23,770	EIVLTQSP (SEQ ID NO: 146)	EIVLTQSP (SEQ ID NO: 146)
CT 6.1.1	1.36	1.3	4 bands	50 & 24 kDa	6 bands	101,100	51,476	23,747	EIVLTQSP (SEQ ID NO: 147)	EIVLTQSP (SEQ ID NO: 147)
* all heavy chains n-terminally blocked (not sequenced in-house)										
** mixed sequence reported: TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145)										
*** mixed sequence observed TGEFVLTQSP (60) (SEQ ID NO: 144) & EFVLTQSP (40) (SEQ ID NO: 145)										

IOD<sub>280nm</sub> = 0.633 mg/ml  
Ec-1.58

Figure 10B

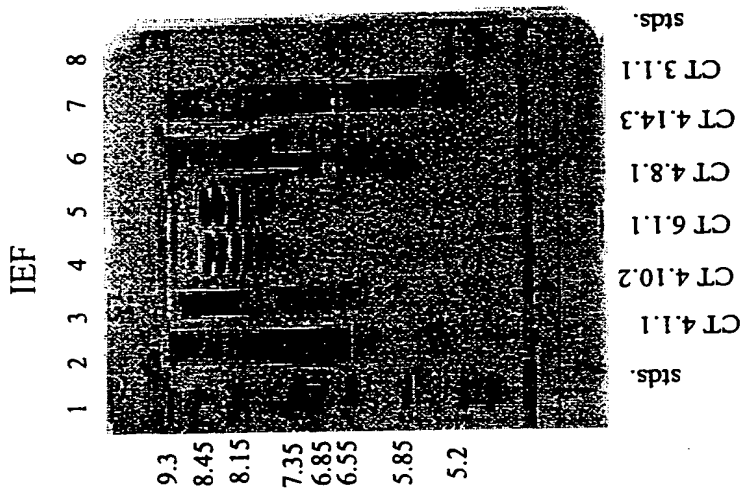


Figure 10C

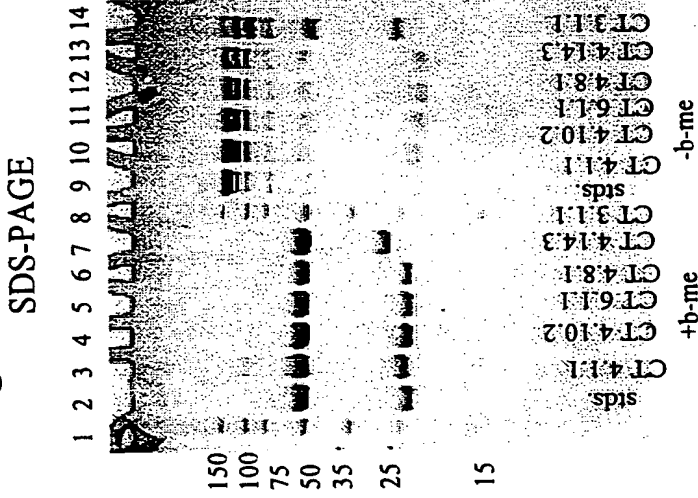
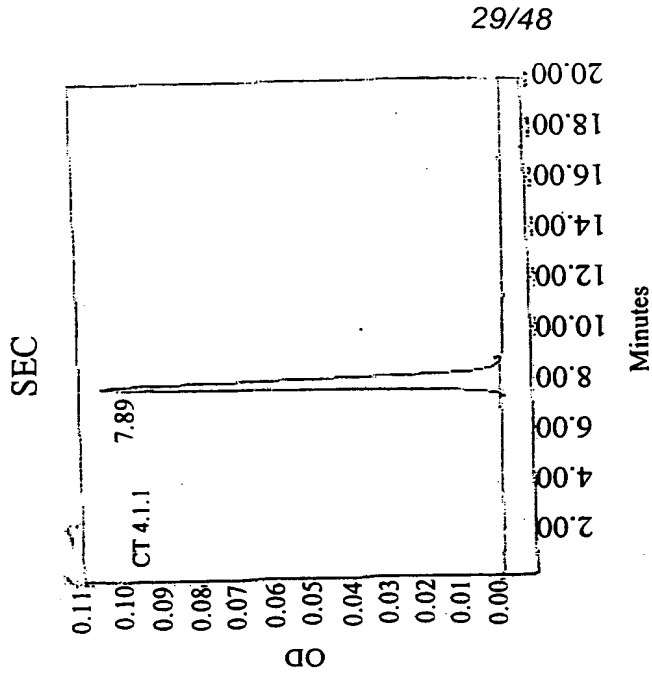
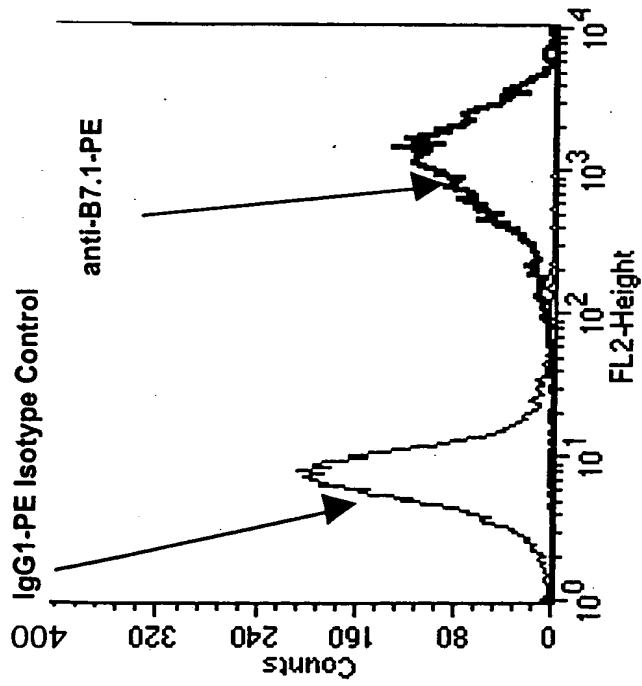


Figure 10D

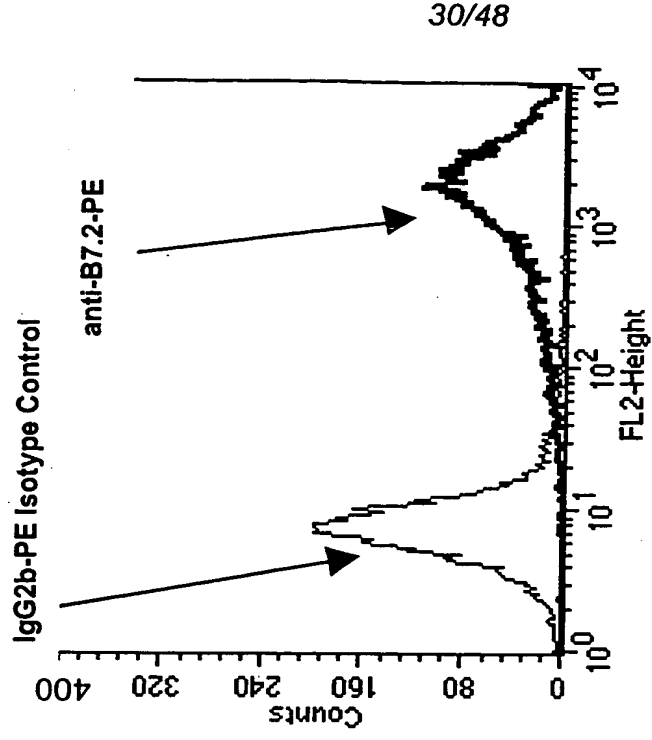


**Figure 11A**



99.7% B7.1 pos.

**Figure 11B**

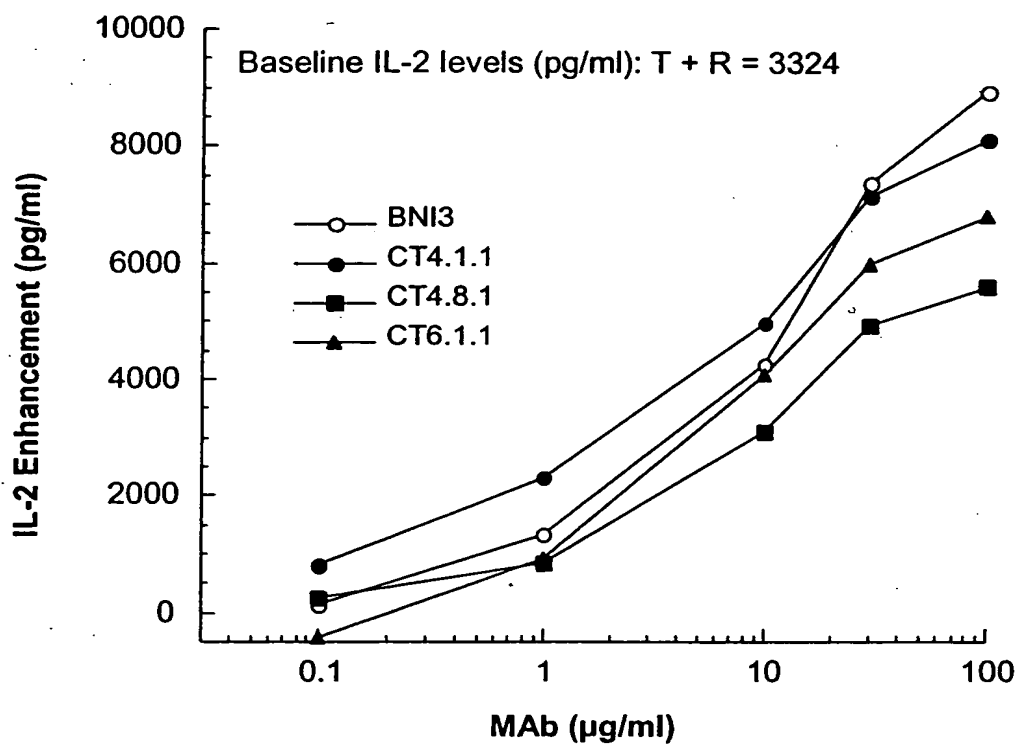


99.7% B7.2 pos.

Expression of B7.1 and B7.2 on Raji Cells

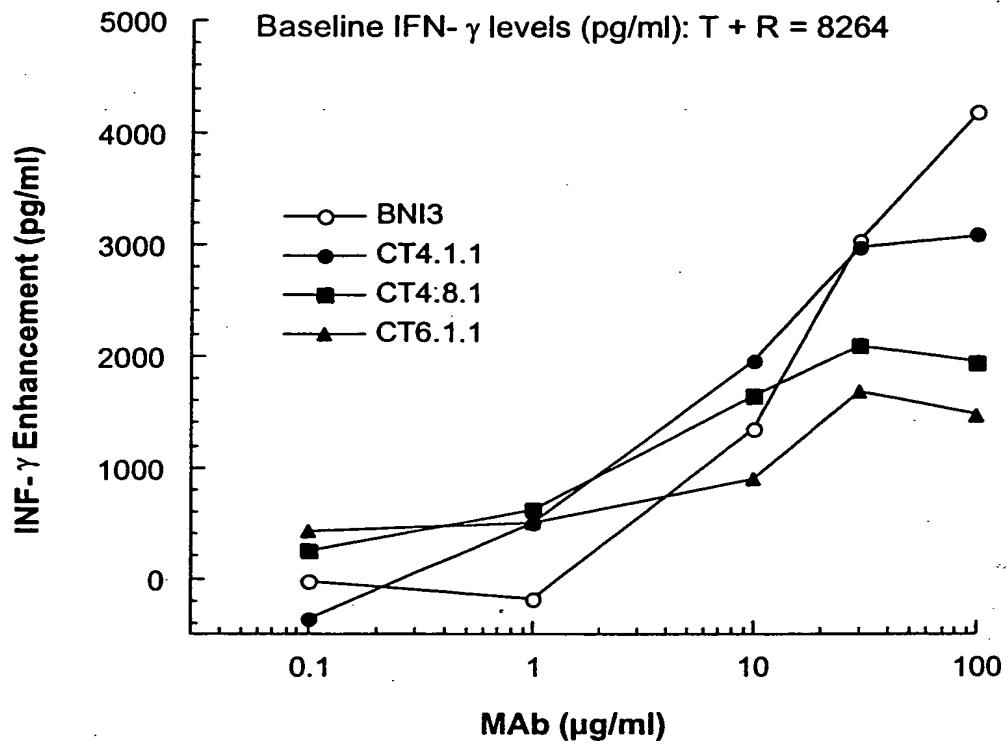
**Figure 12**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 13**

**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay**

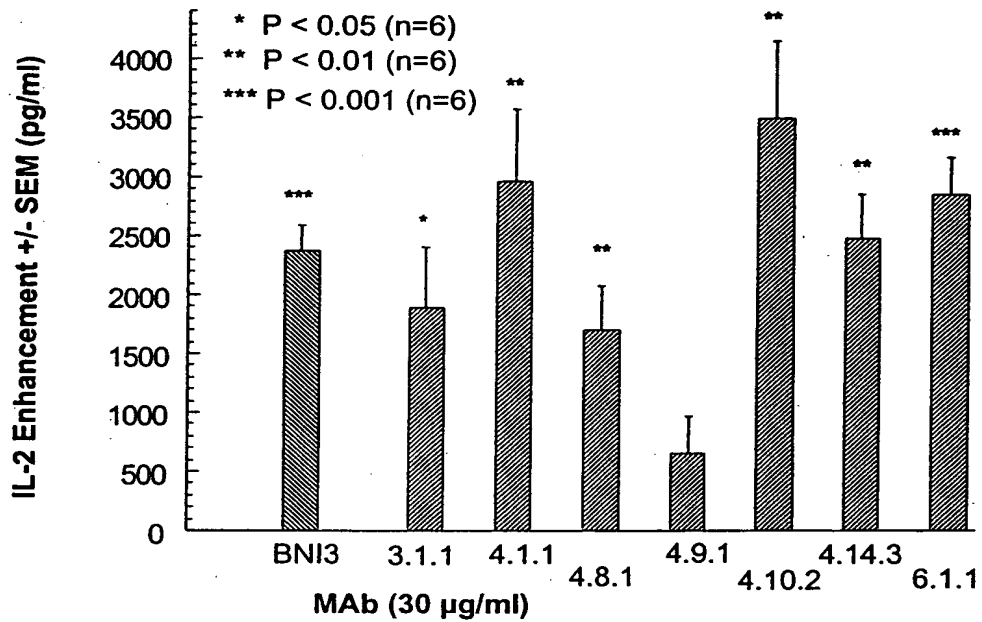




## Figure 14

Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay (6 Donors)

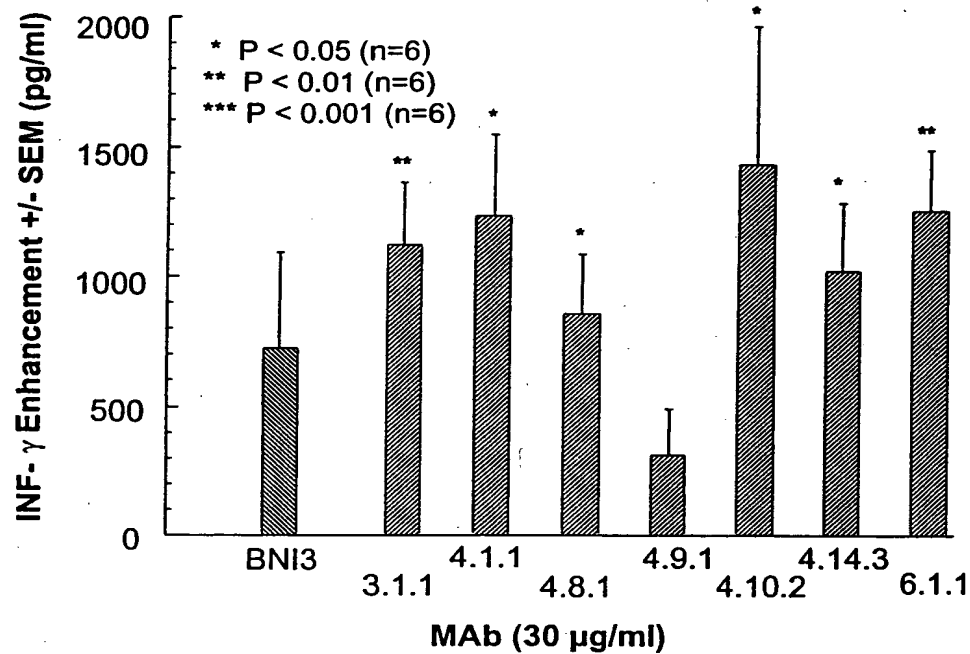
Baseline IL-2 levels (pg/ml): T + R = 9187, T + R + IgG2a = 9389, T + R + IgG2 = 8509



**Figure 15**

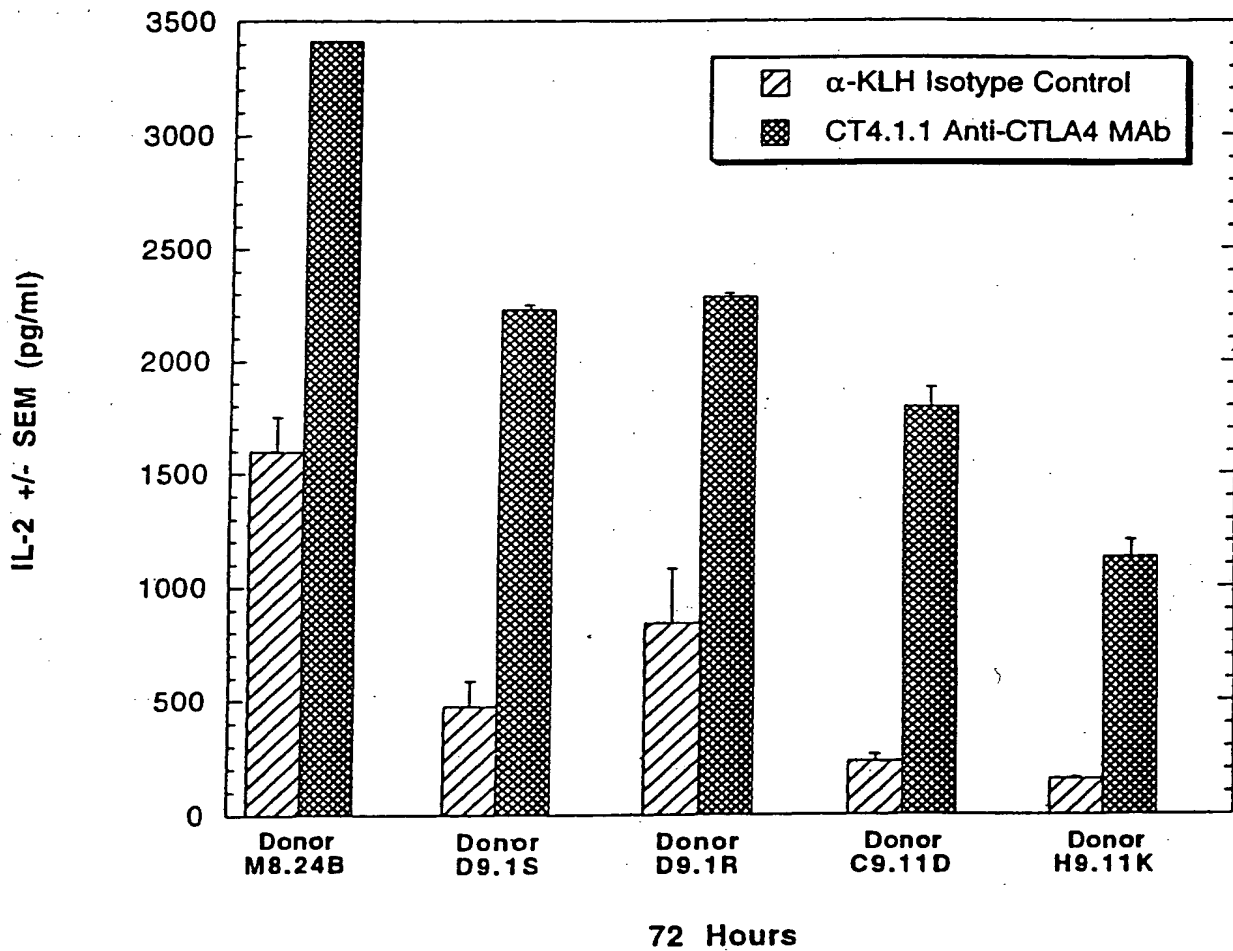
**Enhancement of Human T Cell IFN- $\gamma$  Production  
Induced by Anti-CTLA4 XenoMouse MAbs in  
the 72 Hour T Blast / Raji Assay (6 Donors)**

Baseline IFN- $\gamma$  levels (pg/ml): T + R = 4780, T + R + IgG2a = 4868, T + R + IgG2 = 4331



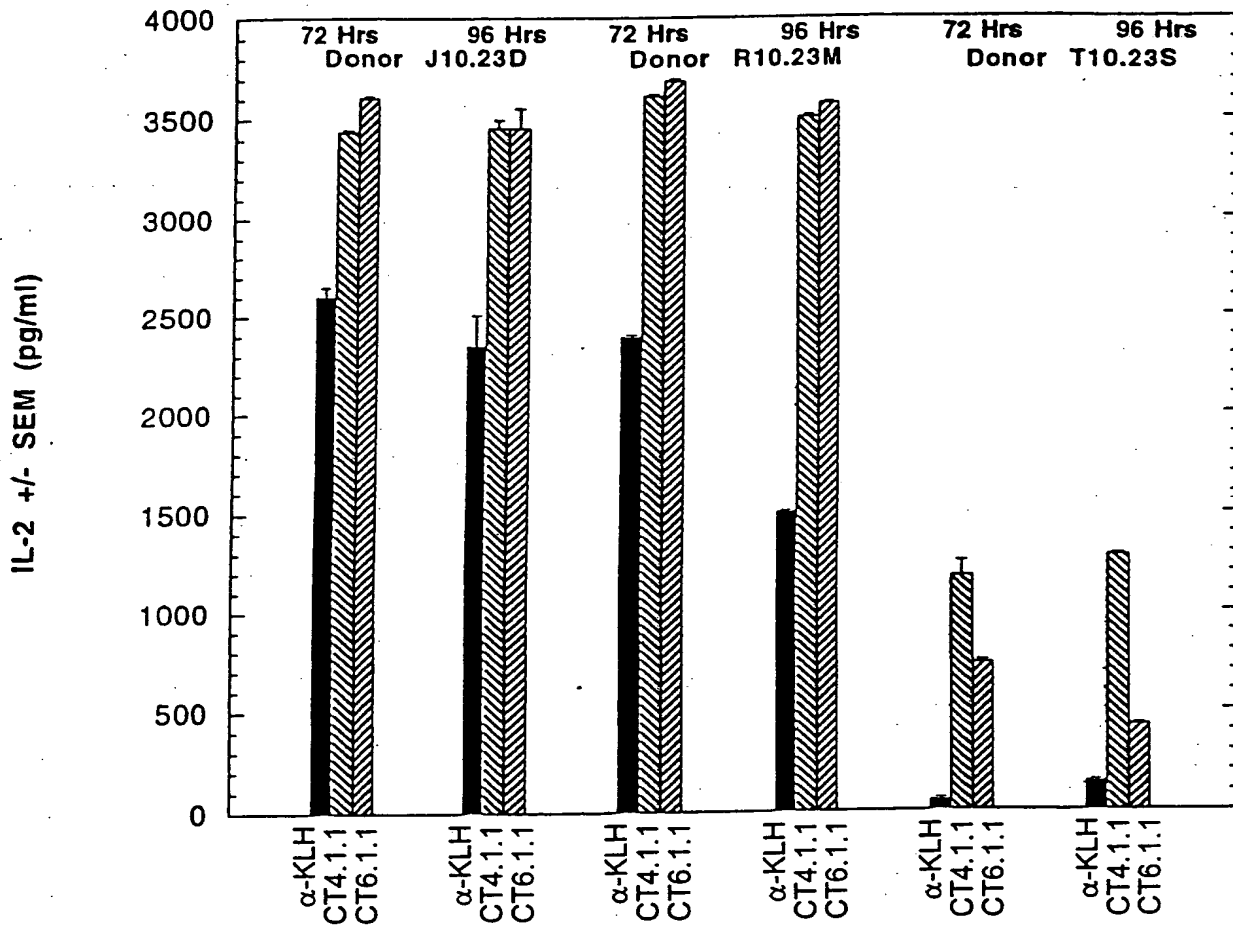
**Figure 16**

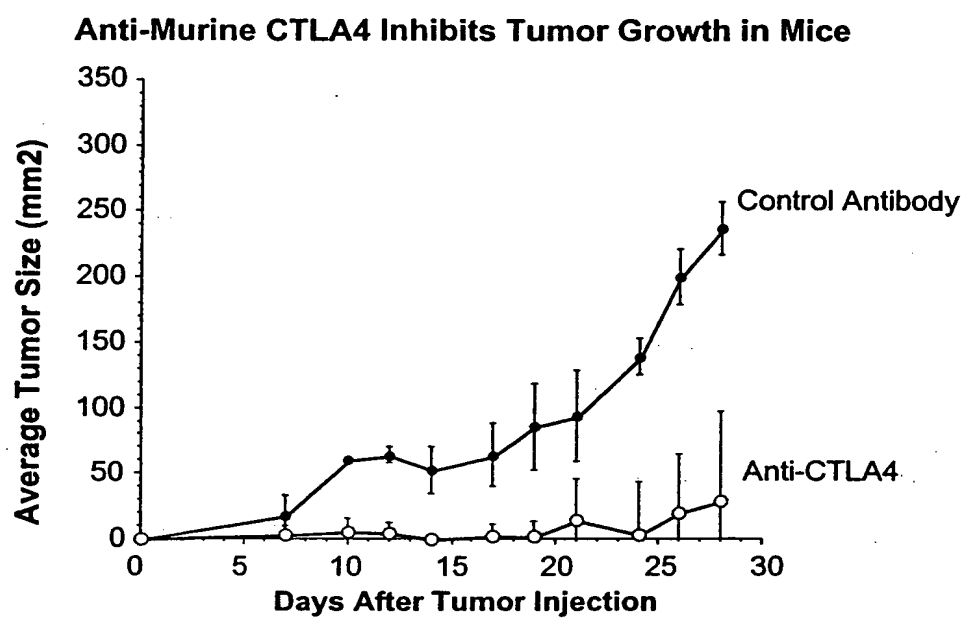
**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAb CT4.1.1 (30  $\mu$ g/ml) Binding to Human PBMC Stimulated with SEA (100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)**



**Figure 17**

**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in Human Whole Blood Stimulated with SEA  
(100 ng/ml) Plus Anti-CD3 MAb (60 ng/ml)**

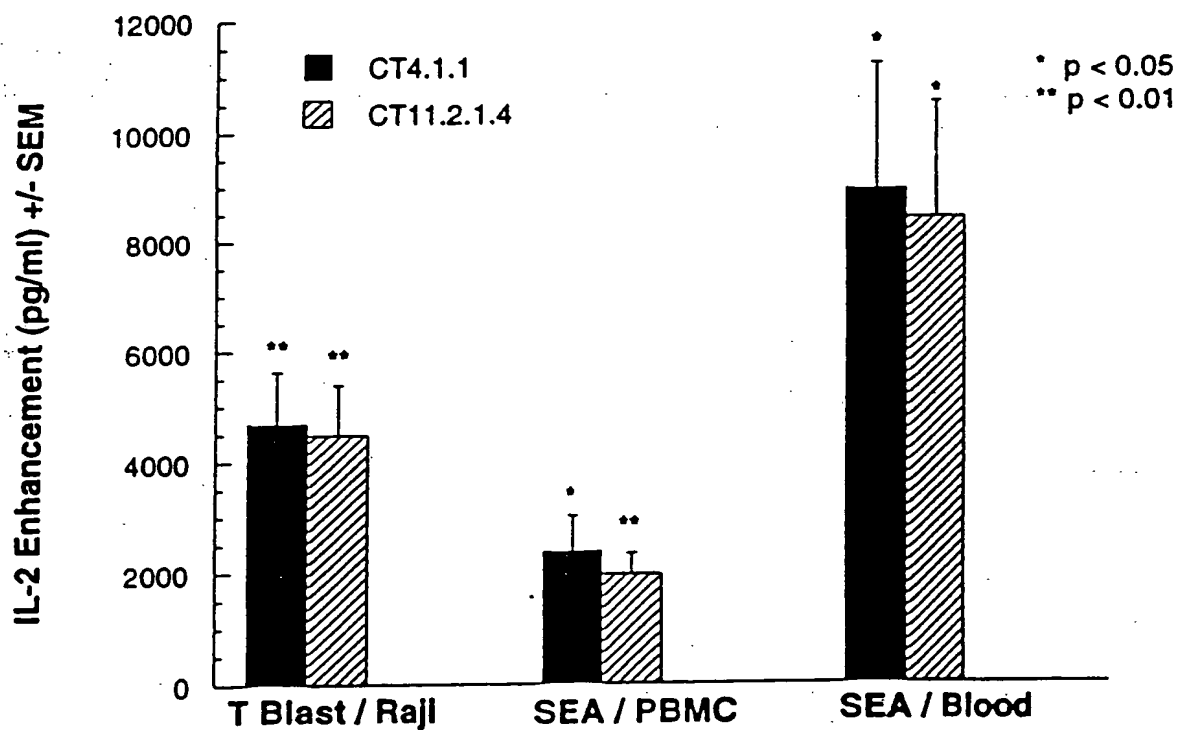


**Figure 18**

Treatment was administered on day  
0,4,7,and 14 after tumor challenge

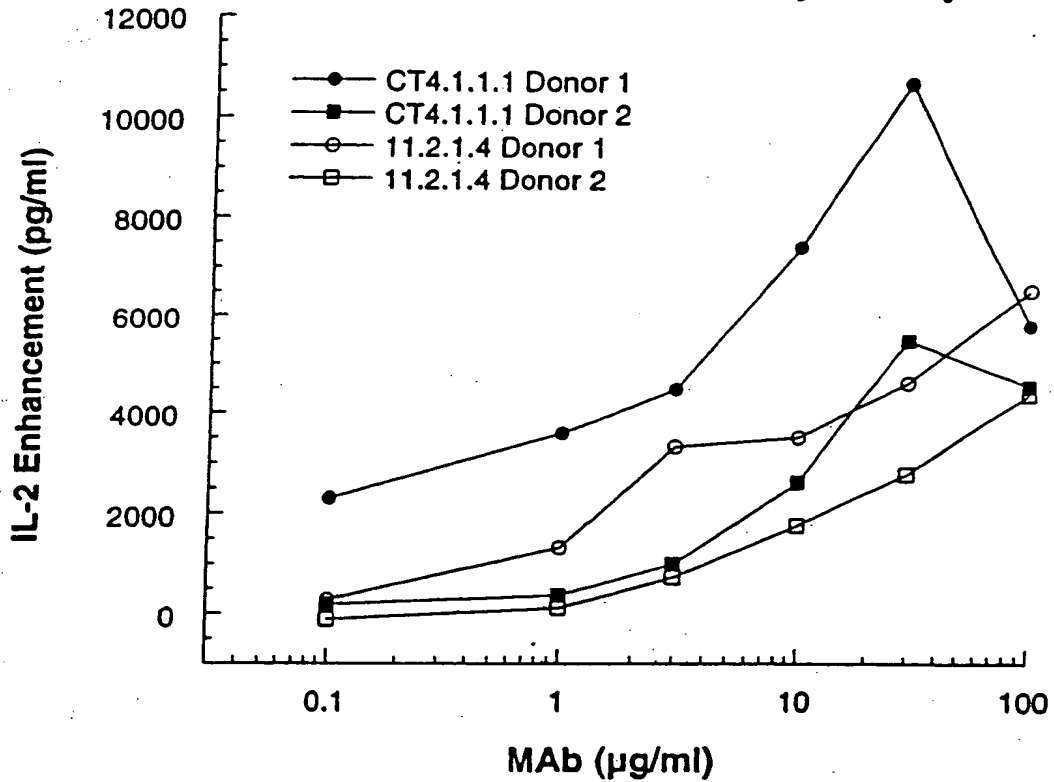
**Figure 19**

**Enhancement of IL-2 Production Induced by Anti-CTLA4 MAbs  
(30  $\mu$ g/ml) in the 72 Hour T Blast / Raji and  
Superantigen Assays (6 Donors)**



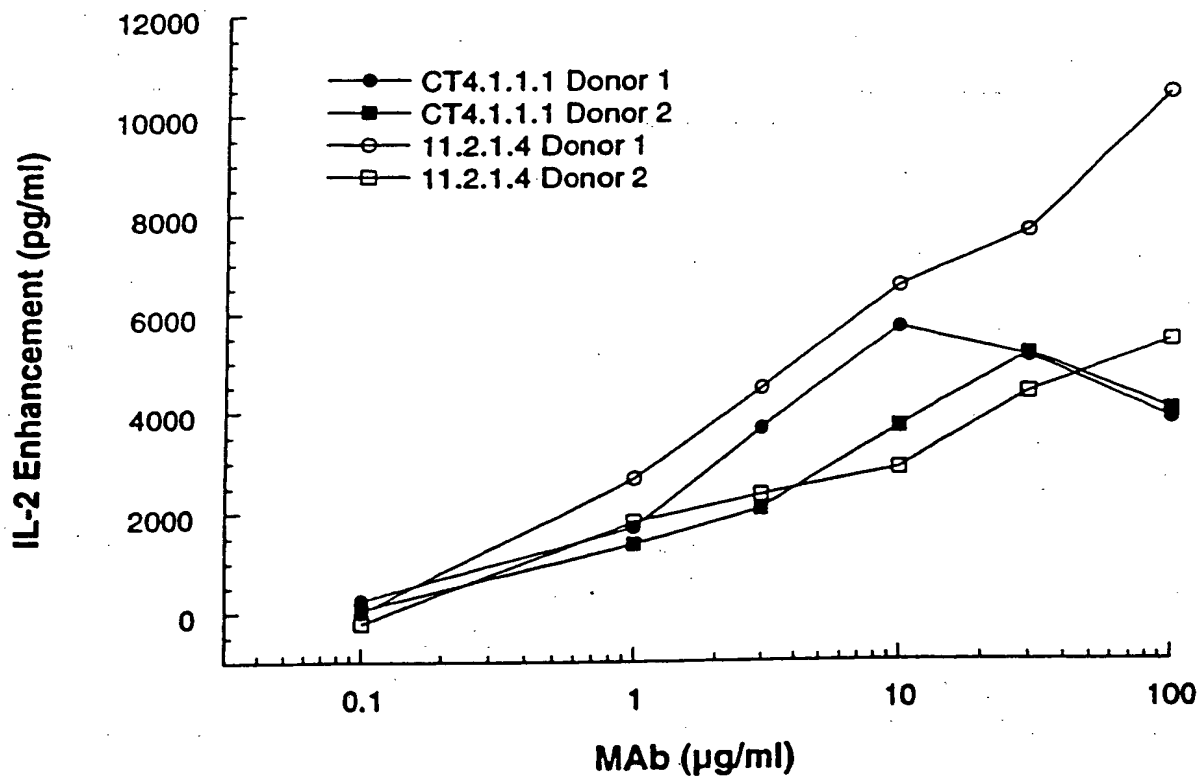
**Figure 20**

**Enhancement of Human T Cell IL-2 Production  
Induced by Anti-CTLA4 MAbs in  
the 72 Hour T Blast / Raji Assay**



**Figure 21**

**Enhancement of IL-2 Production Induced by Anti-CTLA4  
MAbs in Whole Blood Stimulated with  
Superantigen (100 ng/ml)**





- Signal peptides shown in bold and large text
- Open reading frame for genomic clone underlined
- Mutations introduced to make deglycosylated Ab (N294Q) double underlined and large text

**Figure 22A** 4.1.1 IgG2 Heavy Chain cDNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
TGACGGTGTCGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGACACACCTTCCCA  
GCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGCGAGTGCCCA  
CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCCTAAA  
ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACGTGCGTGGTGG  
TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
GTTCCGTGTGGTCAGCGTCCTCACCGTTGTGCACCAGGACTGGCTGAACGGCA  
AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA  
AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
GAGAACAATAACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:53)

**Figure 22B** 4.1.1 IgG2 Heavy Chain Genomic DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCCT  
 TCGGTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCT  
 AGCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGGTGAGAGGCCAGCTCAGGGAGGGAGG  
 GTGTCTGCTGGAAGCCAGGCTCAGCCCTCCTGCCTGGACGCACCCCGGCTGTG  
 CAGCCCCAGCCCAGGGCAGCAAGGCAGGCCCCATCTGTCTCCTCACCCGGAGG  
 CCTCTGCCCCGCCCCACTCATGCTCAGGGAGAGGGTCTTCTGGCTTTTTCACCC  
 AGGCTCCAGGCAGGCACAGGCTGGGTGCCCTACCCAGGCCCTTCACACACA  
 GGGGCAGGTGCTTGGCTCAGACCTGCCAAAAGCCATATCCGGGAGGACCTGC  
 CCCTGACCTAAGCCGACCCCAAAGGCCAAACTGTCCACTCCCTCAGCTCGGAC  
 ACCTTCTCTCCTCCCAGATCCGAGTAACTCCCAATCTTCTCTCTGCAGAGCGC  
 AAATGTTGTGTGCGAGTGCCACCGTGCCAGGTAAGCCAGCCAGGCCTCGCC  
 CTCCAGCTCAAGGCGGGACAGGTGCCCTAGAGTAGCCTGCATCCAGGGACAGG  
 CCCCAGCTGGGTGCTGACACGTCCACCTCCATCTCTTCTCCTCAGCACCACTGT  
 GGCAGGACCGTCAGTCTTCTCTTCCCCCAAACCCAAGGACACCTCATGA  
 TCTCCCCGACCCCTGAGGTACGTGCGTGGTGGTGGACGTGAGCCACGAAGAC  
 CCCGAGGTCCAGTTCAACTGCTACGTGGACGGCGTGGAGGTGCATAATGCCAA  
 GACAAAGCCACGGGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAAGGTCC  
 TCACCGTTGTGCACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTC  
 TCCAACAAAGGCCTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGG  
 TGGGACCCGCGGGGTATGAGGGCCACATGGACAGAGGCCGGCTCGGCCACCC  
 TCTGCCCTGGGAGTGACCGCTGTGCCAACCTCTGTCCCTACAGGGCAGCCCCG  
 AGAACCACAGGTGTACACCCTGCCCCATCCCGGGAGGAGATGACCAAGAACC  
 AGGTGAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTG  
 GAGTCGGAGAGCAATGGGCAGCCGAGAGAACAATAAGACACACCTCCCAT  
 GCTGGAATCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGA  
 GCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTG  
 CACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ  
 ID NO: 54)

**Figure 22C** 4.1.1 IgG2 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSLRLSCVASGFTFSS  
 HGMHWVRQAPGKGLEWVAVIWDGRNKYYADSVKGRFTISRDN SKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWQGTLTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNV DHKPSNTKVDKTV ERKCCVECP PCPAPPVAGPSVFLFPPK  
 PKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVS VLT VVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL P  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT PMLDSDGSFF  
 LYSKLTVDKSRWQQGNV FSCSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO: 63)

**Figure 22D** 4.1.1 IgG2 Heavy Chain cDNA N294Q

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGTAGCGTCTGGATTACCTTCAGTAG  
 CCATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGAAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTCACT  
 TCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCA  
 CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCAAA  
 ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTT**C**C**A**AAGCAC  
 GTTCCGTGTGGTCAGCGTCTCTACCGTTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCC  
 CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTACAGCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAACATAAGACACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:55)

**Figure 22E** 4.1.1 IgG2 Heavy Chain Protein N294Q

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSLRLSCVASGFTFSS  
 HGMHWVRQAPGKGLEWVAVIWDGRNKYYADSVKGRFTISRDN SKNTLFLQMN  
 SLRAEDTAVYYCARGGHFGPFDYWQGTLVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVTP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVVERKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQF**Q**ST  
 FRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLP  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFF  
 LYSKLTVDKSRWQQGNVFS CSVMHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO: 64)

**Figure 22F** 4.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCTGTCT**  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTATTA  
 GCAGCAGCTTCTTAGCCTGGTACCAGCAGAGACCTGGCCAGGCTCCCAGGCTC  
 CTCATCTATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGG  
 CAGTGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAG  
 ATTTTGCAGTGTATTACTGTCAGCAGTATGGTACCTCACCTGGACGTTTCGGC  
 CAAGGGACCAAGGTGGAAATCAAACGAAGTGTGGCTGCACCATCTGTCTTCAT  
 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCC  
 TGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAAC  
 GCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGA  
 CAGCACCTACAGCCTCAGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGA  
 AACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTC  
 ACAAAGAGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:56)

**Figure 22G** 4.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLDPDTTGE**IVLTQSPGTLSSLSPGERATLSCRASQSI  
 SSFLAWYQQRPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPED  
 FAVYYCQYGTSPWTFGQGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCL  
 LNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYLSLSTLTLSKADYEK  
 HKVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:65)

**Figure 22H** 4.8.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAA  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAACACTATGGAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGTGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGAGAGAC  
 TGGGGTCTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCAACCGTCTCCTCA  
 GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCAC  
 CTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAAC  
 CGGTGACGGTGTCTGTGGAAGTCAAGCGCTCTGACCAGCGGCGTGCACACCTTC  
 CCAGCTGTCTTACAGTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGT  
 GCCCTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGC  
 CCAGCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTGTCGAGTGC  
 CCACCGTGGCCAGCACACCTGTGGCAGGACCGTCAGTCTTCTCTTCCCCC  
 AAAACCCAAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTACAGTGCCTGG  
 TGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGAC  
 GGCGTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAG  
 CACGTTCCGTGTGGTCAAGCTCTCACCCTGTGCAACAGGACTGGCTGAACG  
 GCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCAGCCCCCATCGAG  
 AAAACCATCTCCAAAACCAAGGGCAGCCCCGAGAACCACAGGTGTACACCTT  
 GCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGG  
 TCAAAGGCTTCTACCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAG  
 CCGGAGAACAACTACAAGACCACCTCCCATGCTGGACTCCGACGGCTCCTT  
 CTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGGCGGAACG  
 TCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAG  
 AGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:57)

**Figure 22I** 4.8.1 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVQPGRSLRLSCTASGFTFSN  
 YGMHWVRQAPGKGLEWVAVIWDGSGNKHVYDGSVKGRFTISSDNSKNTLYLQMN  
 SLRAEDTAVYYCARGERLGSYFDYWGQGTLLTVSSASTKGPSVFPLAPCSRST  
 SESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTV  
 PSSNFGTQTYTCNVDPKPSNTKVDKTVERKCCVECPPEPPVAGPSVFLFPP  
 KPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNS  
 TFRVSVSLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTL  
 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSF  
 FLYSKLTVDKSRWQQGNVFCFVMSHHEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:66)

**Figure 22J** 4.8.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACACCGG**AGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC  
 TTTGTCTCCAGGGGAAAGAGCCACCCTCTCCTGCAGGACCAGTGTTAGCAGCA  
 GTTACTTAGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATC  
 TATGGTGCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCACTGGCAGTGG  
 GTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATTTTG  
 CAGTCTATTACTGTACGAGTATGGCATCTCACCTTCACTTTCGGCGGAGGG  
 ACCAAGGTGGAGATCAAGCGAACTGTGGCTGCACCATCTGTCTTCATCTTCCC  
 GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGA  
 ATAACCTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTC  
 CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCAC  
 CTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACA  
 AAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAG  
 AGCTTCAACAGGGGAGAGTGTTAG (SEQ ID NO:58)

**Figure 22K** 4.8.1 Kappa Chain Protein

**METPAQLLFLLLLWLPD**TTGEIVLTQSPGTLSSLSPGERATLSCRISVSSS  
 YLAWYQQKPGQAPRLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFA  
 VYYCQQYGISPFTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLN  
 NFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHK  
 VYACEVTHQGLSPVTKSFNRGEC (SEQ ID NO:67)

**Figure 22L** 6.1.1 Heavy Chain DNA

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT**CAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAG  
 CCTGGGAGGTCCCTGAGACTCTCCTGTACAGCGTCTGGATTACCTTCAGTAG  
 TTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGCAATAAACACTATGCAGACTCCGCGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGACTGC  
 TGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCC  
 TCCACCAAGGGCCCATCGGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCACCTC  
 CGAGAGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGG  
 TGACGGTGTCTGTGGAACCTCAGGCGCTCTGACCAGCGGCGTGCACACCTTCCCA  
 GCTGTCTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCC  
 CTCCAGCAACTTCGGCACCCAGACCTACACCTGCAACGTAGATCACAAGCCCCA  
 GCAACACCAAGGTGGACAAGACAGTTGAGCGCAAATGTTGTGTCGAGTGCCCCA  
 CCGTGCCCAGCACCACTGTGGCAGGACCGTCAGTCTTCCTCTTCCCCCAAA  
 ACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACGTGCGTGGTGG  
 TGGACGTGAGCCACGAAGACCCCGAGGTCCAGTTCAACTGGTACGTGGACGGC  
 GTGGAGGTGCATAATGCCAAGACAAAGCCACGGGAGGAGCAGTTCAACAGCAC  
 GTTCCGTGTGGTCAGCGTCTCTACCGTTGTGCACCAGGACTGGCTGAACGGCA  
 AGGAGTACAAGTGCAAGGTCTCCAACAAAGGCCTCCCAGCCCCCATCGAGAAA  
 ACCATCTCCAAAACCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCC  
 CCCATCCCCGGGAGGAGATGACCAAGAACCAGGTGAGCCTGACCTGCCTGGTCA  
 AAGGCTTCTACCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCG  
 GAGAACAACTACAAGACCACACCTCCCATGCTGGACTCCGACGGCTCCTTCTT  
 CCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCT  
 TCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGC  
 CTCTCCCTGTCTCCGGGTAAATGA (SEQ ID NO:59)

**Figure 22M** 6.1.1 Heavy Chain Protein

**MEFGLSWVFLVALLRGVQC**QVQLVESGGGVVEPGRSLRLSCTASGFTFSS  
 YGMHWVRQAPGKGLEWVAVIWDGSKHYADSAKGRFTISRDNKNTLYLQMN  
 SLRAEDTAVYYCARAGLLGYFDYWGQGLTVTVSSASTKGPSVFPLAPCSRSTS  
 ESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVP  
 SSNFGTQTYTCNVDHKPSNTKVDKTVERKCCVECPPCPAPPVAGPSVFLFPPK  
 PKDTLMI SRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNST  
 FRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLF  
 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPMLDSDGSFF  
 LYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLSLSPGK (SEQ ID  
 NO:68)

**Figure 22N** 6.1.1 Kappa Chain DNA

**ATGGAAACCCAGCGCAGCTTCTCTTCCTCCTGCTACTCTGGCTC**  
**CCAGATAACCACCGGAGAAATTGTGTTGACGCAGTCTCCAGGCACCCTGTC**  
 TTTGTCTCCAGGGGAAAGAGCCACCTCTCCTGTAGGGCCAGTCAAAGTGTTA  
 GCAGCTACTTAGCCTGGTACCAACAGAAACCTGGCCAGGCTCCCAGGCCCTC  
 ATCTATGGTGTATCCAGCAGGGCCACTGGCATCCCAGACAGGTTTCAAGTGGCAG  
 TGGGTCTGGGACAGACTTCACTCTCACCATCAGCAGACTGGAGCCTGAAGATT  
 TTGCAGTGTATTACTGTCAGCAGTATGGTATCTCACCATTCACTTTCGGCCCT  
 GGGACCAAAGTGGATATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTT  
 CCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGC  
 TGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGATAACGCC  
 CTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAG  
 CACCTACAGCCTCAGCAGCACCTTGACGCTGAGCAAAGCAGACTACGAGAAAC  
 ACAAGTCTACGCCTGCGAAGTCAACCATCAGGGCCTGAGCTCGCCCGTCACA  
 AAGAGCTTCAACAGGGGAGAGTGTAG (SEQ ID NO:60)

**Figure 22O** 6.1.1 Kappa Chain Protein

**METPAQLLFLLLLWLDPD****T****T****G****E****I****V****L****T****Q****S****P****G****T****L****S****L****S****P****G****E****R****A****T****L****S****C****R****A****S****Q****S****V****S**  
 SYLAWYQQKPGQAPRPLIYGVSSRATGIPDRFSGSGSGTDFTLTISRLEPEDF  
 AVYYCQQYGISPFITFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLL  
 NNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKH  
 KVYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO:69)

**Figure 22P** 11.2.1 IgG2 Heavy Chain DNA:

**ATGGAGTTTGGGCTGAGCTGGGTTTTCTCCTCGTTGCTCTTTTAAGA**  
**GGTGTCCAGTGT****C****A****G****G****T****G****C****A****G****C****T****G****G****T****G****G****A****G****T****C****T****G****G****G****G****A****G****G****C****G****T****G****G****T****C****C****A****G**  
 CCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCGTCTGGATTACCTTCAGTAG  
 CTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTGG  
 CAGTTATATGGTATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGC  
 CGATTACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAA  
 CAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGAGGG  
 GAGCTACCCCTTTACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACC  
 ACGGTACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC  
 GCCCTGCTCCAGGAGCACCTCCGAGAGCACAGCGGCCCTGGGCTGCCTGGTCA  
 AGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCTCTGACC  
 AGCGGCGTGACACACCTTCCAGCTGTCTTACAGTCTCAGGACTCTACTCCCT  
 CAGCAGCGTGGTGACCGTGCCCTCCAGCAACTTCGGCACCCAGACCTACACCT  
 GCAACGTAGATCACAAGCCCAGCAACACCAAGGTGGACAAGACAGTTGAGCGC  
 AAATGTTGTGTCGAGTGCCACCGTGCCAGCACCACCTGTGGCAGGACCGTC  
 AGTCTTCCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCC  
 CTGAGGTACGTCGCTGGTGGTGGTGGACGTGAGCCACGAAGACCCCGAGGTCCAG  
 TTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCACG  
 GGAGGAGCAGTTCAACAGCACGTTCCGTGTGGTCAGCGTCCTCACCGTTGTGC  
 ACCAGGACTGGCTGAACGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGGC  
 CTCCCAGCCCCCATCGAGAAAACCATCTCCAAAACCAAAGGGCAGCCCCGAGA  
 ACCACAGGTGTACACCTTGCCCCCATCCCCGGAGGAGATGACCAAGAACCAAG  
 TCAGCCTGACCTGCCTGGTCAAAGGCTTCTACCCAGCGACATCGCCGTGGAG  
 TGGGAGAGCAATGGGCAGCCGGAGAACAATAACAAGACCACACCTCCCATGCT  
 GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA  
 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCAC  
 AACCATAACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGA (SEQ ID  
 NO:61)

**Figure 22Q** 11.2.1 IgG2 Heavy Chain Protein:

QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWIY  
 DGSNKYYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCARDPRGATLY  
 YYYYGMDVWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP  
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDH  
 KPSNTKVDKTVKCCVECPPCPAPPVAGPSVFLFPPKPKDTLMISRTPEVTC  
 VVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWL  
 NGKEYKCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSREEMTKNQVSLTC  
 LVKGFYPSDIAVEWESNGQPENNYKTTPMLDSDGSFFLYSKLTVDKSRWQQG  
 NVFSCSVMEALHNHYTQKSLSLSPGK (SEQ ID NO:70)

**Figure 22R** 11.2.1 IgG2 Kappa Chain DNA:

ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTACTC  
 TGGCTCCGAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCCT  
 CCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCACTTGCCGGGCAAGTCAG  
 AGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCAGGGAAAGCCCCTAA  
 ACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA  
 GTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT  
 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTT  
 CGGCCCTGGGACCAAAGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCT  
 TCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTG  
 TGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGGA  
 TAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCA  
 AGGACAGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTAC  
 GAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCC  
 CGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTGA (SEQ ID NO:62)

**Figure 22S** 11.2.1 IgG2 Kappa Chain Protein:

DIQMTQSPSSLSASVGDRVTITCRASQSINSYLDWYQQKPGKAPKLLIYAASS  
 LQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCQYYSTPFTFGPGTKVEI  
 KRTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNS  
 QESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRG  
 EC (SEQ ID NO:71)



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